

0072274120400

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TCACGCGTCCGGTCAAGCTCTCTTTCGAGAGAAGCAAGCGGCTGGCGTGGGCCATCCGGGGAATGGGC
GCGCTCTGACCTAGTGTTCGCGGGGCAAAAAGGGTCTTTCGCGGCTCGCTCGTGCAGGGGCTAT
TTGGGCGCCTGAGCGCGGCGTGGAGCCTTGGAGCCGCGCGCAGCAGGGGGCACACCCGGAACCG
GCTCAGCGCGCGGACCATGACCGGGAGGCCATCTCAGCGCCCTGCCACCATTCCTTACCA
CAAACTGCGCGACCTGCGCTACCTGAGCCGCGGCGCTCTGGCACTGTGTCTCGTCCGCGCGCACG
CAGACTGGCGCGTCCAGGTGGCGCTGAAGCACCTGCACATCCACACTCGGCTGCTGCACAGTGAA
AGAAAGCATGTCTTAAGAGAAGCTCAAAATTTTACACAAAGCTAGATTAGTTACATTCCTTCAAT
TTGGGGAATTTCAATGAGCGCTCAATTTTGGGAATAGTTACTGAATACATGCCAATGCAATCAT
TAAATGAACCTCTACATAGGAAAACCTAATATCCTGATGTTGCTTGGCCATTGAGATTTCTATC
CTGCATGAAATTCGCGCTTGGTGTAAATTACCTGCACAATATGACTCCTCCTTTACTTCATCATGA
CTTTAGACTCAGAATATCTTATTCGACAATCAATTTCAATGTTAAGATTGCAGATTTTGGTTTAT
CAAGTGGCGCATGATGTCTCTCAGAGTCACGAAGTAGCAAAATCTGCACGAGAAGGAGGGACA
ATTATCTATATGCCACCTGAAAACCTATGAACCTGGACAAAATCAAGGGCCAGTATCAAGCACGA
TATATATAGCTATGCAGTTATCAGATGGGAAGTGTATCCAGAAAACAGCCTTTTGAAGATGTCA
CCAATCCTTTGCAGATAATGTATAGTGTGTACAGGACATCGACCTGTTATTAATGAAGAAAGT
TTGCCATATGATATACCTCACCCAGCACGTATGATCTCTCTAATAGAAAGTGGATGGGCACAAAA
TCCAGATGAAAGACCATCTTTCTTAAAAATGTTTATAGAACTTCAACCAGTTTTGAGAACATTTG
AAGAGATAACTTTCTTGAAGCTCTTATTCAGCTAAAGAAAACAAAGTTACAGAGTGTTCAGT
GCCATTCACTATGTGACAGAAGAAAAATGGAATTTCTCTCAACATACCTGTAATCATGGTCC
ACAAGAGGAATCATGTGGATCTCTCAGCTCCATGAAAATAGTGGTTCTCTGAAAACCTCAAGGT
TCTTGGCAGCTCTCTCAGACAAATGATTTTCTTCTAGAAAAGCTCAGACTGTCTATTTATGAAG
CTGCATCACTGTCTCTGGAAATCAGAGTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATT
CTGTGATCACAAGACCATTTCTATGCTCTTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACT
CAGAACGTCTGCAAGCCTGGTATAGCCGAGCAGTGGATCCAGAGCAAAAAGGGGAAGACATTGTGAAC
CAAAATGACAGAAGCCTGCGCTTAACCAAGTGGCTAGATGCCCTTCTGTCCAGGGGACTTCAATCATGAA
AGAGGACTATGAACCTGTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAAATTACTAGACA
CTACTGACATCCAAAGGAGAAGAAATTTGCCAAAGTTTATAGTACAAAAATTGAAAGTATCAACAA
ATGGGTCTTTCAGCCTTACCCGAAATACTTGTGGTTTCTAGATCACCATCTTAAATTTACTTCA
AAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAGAAATGTGTTTCATAAAAGGATATTTATAAA
AA (SEQ ID NO:1)

FIG. 1

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Met	Asn	Gly	Glu	Ala	Ile	Cys	Ser	Ala	Leu	Pro	Thr	Ile	Pro	Tyr	His	Lys	Leu	Ala	Asp	20
Leu	Arg	Tyr	Leu	Ser	Arg	Gly	Ala	Ser	Gly	Thr	Val	Ser	Ser	Ala	Arg	His	Ala	Asp	Tyr	40
Arg	Val	Gln	Val	Ala	Val	Lys	His	Leu	His	Ile	His	Thr	Pro	Leu	Leu	Asp	Ser	Gln	Arg	60
Lys	Asp	Val	Leu	Arg	Glu	Ala	Gln	Ile	Leu	His	Lys	Ala	Arg	Phe	Ser	Tyr	Ile	Leu	Pro	80
Ile	Leu	Gly	Ile	Cys	Asn	Glu	Pro	Glu	Phe	Leu	Gly	Ile	Val	Thr	Glu	Tyr	Met	Pro	Asn	100
Gly	Ser	Leu	Asn	Glu	Leu	Leu	His	Arg	Lys	Thr	Glu	Tyr	Pro	Asp	Val	Ala	Thr	Pro	Leu	120
Arg	Phe	Arg	Ile	Leu	His	Gln	Ile	Ala	Leu	Gly	Val	Asn	Tyr	Leu	His	Asn	Met	Thr	Pro	140
Pro	Leu	Leu	His	His	Asp	Leu	Lys	Thr	Gln	Asn	Ile	Leu	Leu	Asp	Asn	Gln	Phe	His	Val	160
Cys	Ile	Ala	Asp	Phe	Gly	Leu	Ser	Lys	Trp	Arg	Met	Met	Ser	Leu	Ser	Gln	Ser	Arg	Ser	180
Ser	Lys	Ser	Ala	Pro	Glu	Gly	Gly	Thr	Ile	Ile	Tyr	Met	Pro	Pro	Glu	Asn	Tyr	Gln	Pro	200
Gly	Gln	Lys	Ser	Arg	Ala	Ser	Ile	Lys	His	Asp	Ile	Tyr	Ser	Tyr	Ala	Val	Ile	Thr	Trp	220
Gln	Val	Leu	Ser	Arg	Lys	Gln	Pro	Phe	Glu	Asp	Val	Thr	Asn	Pro	Leu	Gln	Ile	Met	Tyr	240
Ser	Val	Ser	Gln	Gly	His	Arg	Pro	Val	Ile	Asn	Glu	Glu	Ser	Leu	Pro	Tyr	Asp	Ile	Pro	260
His	Arg	Ala	Arg	Met	Ile	Ser	Leu	Ile	Gln	Ser	Gly	Trp	Ala	Gln	Asn	Pro	Asp	Gln	Arg	280
Pro	Ser	Phe	Leu	Lys	Cys	Leu	Ile	Glu	Leu	Glu	Pro	Val	Leu	Arg	Thr	Phe	Glu	Gln	Ile	300
Thr	Phe	Leu	Glu	Ala	Val	Ile	Gln	Leu	Lys	Lys	Thr	Lys	Leu	Gln	Ser	Val	Ser	Ser	Ala	320
Ile	His	Leu	Cys	Asp	Lys	Lys	Lys	Met	Glu	Leu	Ser	Leu	Asn	Ile	Pro	Val	Asn	His	Gly	340
Pro	Gln	Glu	Glu	Ser	Cys	Gly	Ser	Ser	Gln	Leu	His	Glu	Asn	Ser	Gly	Ser	Pro	Gln	Thr	360
Ser	Arg	Ser	Leu	Pro	Ala	Pro	Gln	Asp	Asn	Asp	Phe	Leu	Ser	Arg	Lys	Ala	Gln	Asp	Cys	380
Tyr	Phe	Met	Lys	Leu	His	His	Cys	Pro	Gly	Asn	His	Ser	Trp	Asp	Ser	Thr	Ile	Ser	Gly	400
Ser	Gln	Arg	Ala	Ala	Phe	Cys	Asp	His	Lys	Thr	Ile	Pro	Cys	Ser	Ser	Ala	Ile	Ile	Asn	420
Pro	Leu	Ser	Thr	Ala	Gly	Asn	Ser	Gln	Arg	Leu	Gln	Pro	Gly	Ile	Ala	Gln	Gln	Trp	Ile	440
Gln	Ser	Lys	Arg	Glu	Asp	Ile	Val	Asn	Gln	Met	Thr	Gln	Ala	Cys	Leu	Asn	Gln	Ser	Leu	460
Asp	Ala	Leu	Leu	Ser	Arg	Asp	Leu	Ile	Met	Lys	Glu	Asp	Tyr	Glu	Leu	Val	Ser	Thr	Lys	480
Pro	Thr	Arg	Thr	Ser	Lys	Val	Arg	Gln	Leu	Leu	Asp	Thr	Thr	Asp	Ile	Gln	Gly	Glu	Glu	500
Phe	Ala	Lys	Val	Ile	Val	Gln	Lys	Leu	Lys	Asp	Asn	Lys	Gln	Met	Gly	Leu	Gln	Pro	Tyr	520
Pro	Glu	Ile	Leu	Val	Val	Ser	Arg	Ser	Pro	Ser	Leu	Asn	Leu	Leu	Gln	Asn	Lys	Ser	Met	540

(SEQ ID NO:2)

FIG. 2

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TTTTATGGG AATCCGAGCT TGAAGAGAC AGARCAATTC CAGAANTAAA TTERAATTC
 AGATTTACCC AATGTTGTTT TAAAATATTC TAACTTCAAA GAATGATGCC AGAAGTTTAA
 AAGGACCTCC GCAGAGTAGC AGGGGCGCTT GAGGGCGCGG CCTGAATCCT GATTGCCCTT
 TTCTCAGAG GACACAGCCA GCTCAGATG AATTTCGGAA AAGTAGCCGC TTGCTACTTT
 TACTATGGAA GAGCAGGGCC ACAGTGAGAT GGAATAATC GCATCAGAGT CTCACCCCA
 CATTCAATTA CTGAAAAGCA ATCGGGAAT TTTGGTCACT CACATCCSCA ATACTCAGTG
 TCTGGTGGAC AACTTCTCA AGAATGACTA CTTCTCGGCC GAAGATGCCG AGATTGTGTG
 TCCCTGCCCC ACCCAGCCTG ACAAGGTCCG CAAAATTCTG GACCTGCTAC AGAGCAAGGG
 CGAGGAGGTG TCCGAGTTCT TCTCTACTTT GCTCAGCAA CTGGCAGATG CCTACGTGGA
 GCTCAGGCTT TGGCTGCTGG AGATCGGCTT CTGGGCTTCC CTGCTCACTC AGAGCAAGT
 GCTGGTCAAC ACTGACCCAG TTAGCAGGTA TACCCAGCAG CTGGCAGACC ATCTGGGCGG
 TCACTCAAG TCTGTGCTTT GCTATGCCCA GAAGGAGGAG CTGCTGCTGG AGGAGATCTA
 CATGACACC ATCATGGAGC TGGTGGCTT CAGCAATGAG AGCCTGGCCA GCTCAACAG
 CCTGGCCTGC CTCTCGACC ACACACCCCG CATCTCAAT GAGCAGGGTG AGACCATCTT
 CATCTCGGT GATGCTGGGG TGGGCAAGTC CATGCTGCTA CAGCGGCTGC AGAGCCTTGG
 GGGCAGGSC CGGCTAGAGC CAGGGGTCAA ATTCTTCTTC CACTTTGCTT GCGCGATGTT
 CAGCTGCTTC AAGGAAAGTG ACAGGCTGTG TCTGCAGGAC CTGCTCTTCA AGCACTACTG
 CTACCCAGAG CCGGACCCCG AGGAGGTGTT TCCCTTCTTG CTGCGCTTCC GGCACGTGGC
 CCTCTTCACC TTGATGGCC TGGACGAGCT GCACTCGGAC TTGGACCTCA GCGCGGTGGC
 TACAGCTCC TCCGCTGGG AGCCTGSCCA GCGGCTGGTC TTGCTGGCCA ACCTGCTCAG
 TGGGAAGCTG CTGAAGGGGG CTAGCAAGCT CCTCAGGCC GGCACAGGCA TTAGGTGCC
 GCGCCAGTTC CTGCGGAAGA AGGTGCTTCT CCGGGGCTTC TCCCCAGCC ACCTGCGCGC
 CTATGCCAGG AGGATGTTCC CCGAGCGGCG CTTGCAGGAC CGCTGCTGA GGCAGCTGGA
 GGGCAACCCC AACCTCTGCA GCTGTGCTG TGTGCCCCTC TTCTGCTGGA TCACTCTCGG
 GTGCTTCAG CACTTCCCTG CTGCTTTTCA AGGCTCACCA CAGCTGCCCC ACTGCACGAT
 GACCTGACA GATGCTTCC TCTGGTCACT TAGGTCCAT CTGAACAGGA TGCAGCCCG
 CAGCCTGGTG CAGCGGAACA CAGCAGCCC AGTGGAGACC CTCCACGCCG GCGGGGACAC
 TCTGTGCTCC CTGGGGCAGG TGGCCACCG GGGCATGGAG AAGAGCCTCT TTGTCTTCA
 CCAGGAGGAG GTGCAGGCTT CCGGGCTGCA GGAGAGAGAC ATGCAGCTGG GCTTCTGCTG
 GCGTTTCCCG GAGCTGGGCG CCGGGGTGA CCGCAGTCC TATGAGTTT TCCACCTCAG
 GCTCAGGCC TTCTTACAG CCTTCTCTCT CTTGCTGGAC GACAGGGTGG GCACTCAGGA
 GCTGCTCAGG TTCTTCCAGG AGTGGATGCC CCGTCCGGGG GCAGCGACCA CCTCTCTCTA

FIG. 3 (page 1 of 2)

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TCTTCCCTTC CTCCGCTTCC AGTGCCTTCA GGGCAGTGGT CCGGCGCGGG AAGACCTCTT
 TAAGAACAAG GATCACTTCC AGTTCAACCA COTCTTCTG TCGGGCTGT TGTCCAAAGC
 TAAACAGAAA CTCTTCCGGC ATCTCTTCC CCGGCGAGCC CTCAGGAGAA AGCGCAAGGC
 CTCTTGGGCA CACCTCTTTT CCGGCTTCC GGGCTACCTG AAGAGCTTCC CCGGCTTCA
 CTCTCAAAGC TTCAACCAAG TCGAGGCTAT GCGCAGCTT ATCTGGATGC TCGGCTTCA
 TTAGCAGACA CAGAGCCAGA AGGTGGGGCA GCTGGGGGGC AGGGGCTAT CCGCCAACTA
 CTCTAGCTG ACCTACTTCA AGGCTCTCTC CCGGCTTCC AGGCGCTCT CTTTCTCTCT
 GCATCACTTC CCGAAGCGGC TCGGCTTCA CTTAGACAAC AACAATCTCA ACGACTACGG
 CCGTGGGGAG CTTCAGGCTT GCTTCAAGCC CTTCACTCTT CTCAGACTCA GCGTAAACCA
 GATCACTGAC GGTGGGGTAA AGGTGCTTAA CCAAGAGCTG ACCAATACA AAATTCTGAC
 CTATTCTGGT TTATACAACA ACCAGATCAC CCACTCTTCA GCGAGGTACG TCACCAAAAT
 CTCTGATGAA TCAAAAGGCC TCGGCTTCT TAACTCTTCA AAAACAAAA TAACAAGTCA
 AGGAGGGAAG TATCTCGGCC TCGGCTTCA GAACAGCAAA TCAATCTCT AGGTCTGGAT
 CTGGGGCAAT CAAGTTGGGG ATGAAGGAGC AAAAGCCTTC GCAGAGGCTC TCGGGAACCA
 CCGCAGCTTC ACCACCTTCA GTTCTCTCTC CAACGGCTTC TCCACAGAAG GAGGAAAGAG
 CTTTCTGAGG GCGCTTCCAG AGAAGCTTC TCTAGAAATA CTCTGGCTCA CCGAAATCA
 ACTCAACCAT CAAGTGGCAG AGAGTTTGGC AGAAATGTTG AAAGTCAACC AGACGTTAAA
 GCATTTATGG CTTATCCAGA ATCAGATCAC AGCTAAGGGG ACTGCGCCAGC TCGCAGATGC
 GTTACAGAGC AACACTGGCA TAACAGAGAT TTGCTTAAAT GGAACCTTCA TAAACCCAGA
 TGAGGCCAAA GTCTATGAAG ATGAGAAGCG GATTATCTCT TTCTGAGAGG ATGCTTTCTT
 CTCTATGGGG TTTTTCCTCT CCGGCTTTC CAGCAAAATGC CACTCTGGGC AGTCTTTCTT
 CTCAGTCTCT TAAAGGGGCC TCGGCGAGCG GAGCTATCAG GAGTCCACTG CTTTCATGAT
 GCAAGCCAGC TTCTCTTCCA GAAGTCTCTG TCGGCAAACT CCTAAGTAC CCGCTACAA
 TCTGCAGAAA AAGAATGTGT CTTGCGAGCT GTTGTAGTTA CAGTAAATAC ACTGTGAAGA
 GAAAAAAAAA ACGGACGCGT GG (SEQ ID NO:7)

FIG. 3 (page 2 of 2)

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MEEQGHSEMEIIPSESHPHIQLLKSNRELLTTHIRNTQCLVONLLKNDYFSAEDRETVCACTQP
DKVRKILDLVQSKGEEVSEFFLYLLOQLADAYVDLRPWLLLEIGFSPSLLTQSKVWNTDPVSRYT
QQLRHHLGRDSKFVLCIAQKEELLEETIMDTIMELVGFSNESLGSLSLACLLDHTTGILNEQG
ETITILGDAGVGKSMILLQRLQSLWATGRLDAGVKFFTHFRCRMFSCKESDRLCLQDLLFKHYCY
PERDPEEVFAFLLRFPHVALLFTFDGLDELHSELDLSRVPDSSCPWEPAPLVLNLLSGKLLKG
ASKLLTARTGIEVPRQFLRKKVLLRGFSFPHLAYARRMFPERALQDRLLSOLANPNLCSLCSV
PLFCNIIIFRCFQHFRAAFEGSPQLPDCTMTLTDFVLLVTEVHLNRMQPSSSLVQRNTRSPVETLHA
GRDTLCSLGQVAHRGMEKSLFVFTQEEVQASGLQERDMQLGFLRALPELGFGGDCQSYEFFHLTL
CAFFTAFFLVLDLDRVGTQCELLRFFQEWMPFAGAATTSCYFFFLPFQCLQGSGPAREDLFANKDHF
QFTNLFLCGLLSKAKQKLLRHLPAAALRRKXKALNAHLFSSLRGYLKSLPRVQVESFNQVQAMP
TFIWMRLCIVETQSQKVGQLAARGICANYLKLTVCNACSADCSALSFVLHHFPKRLALDLENNNL
NDYGVRELQPCFSRLTVLRLSVNQITDGGVKVLSEELTKYKIVTYLGLYNNQITDVGARYVTKIL
DECKGLTHLKLGGKNKITSEGGKYLALAVKNSKSISEVGMWGNQVGDGAKAFAEALRNHPSLITL
SLASNGISTEGGKSLARALQQNTSLEILNLTQNELNDEVAESLAEMLKVNQTLKHLWLIONQITA
KGTALADALQSNTGITEICLNGNLKPEEAKVYEDEKRIICF (SEQ ID NO:8)

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TACGGCTCCGACTTCTGAGAAATGACTACTTCTCGGCCAAGATGCGGAGATTGTGT
TTGCCCTGCCCCACCCAGCCTGACRAGGTCCGCAAAATTCTGGACCTGGTACAGAGCAAG
GGGAGGAGGTGTCCGAGTTCTTCTCTACTTGTCTCAGCAACTGCGAGATGCCTACGT
GGACCTCAGGCCTTGGCTGCTGAGATCGGCTTCTCCCTTCCCTGCTCACTCAGAGCA
AGTCTGTGGTCAACACTGACCCAGTGGAGAGGTATACCCAGCAGCTGCGACACCATCTG
GGCCTGACTCCAAGTTCTGTCTGTGCTATGCCAGAAGGAGGAGCTGCTGCTGGAGGA
TATCTACATGGACACCATCATGGAGCTGGTGGCTTCAGCAATGAGAGCCTGGGCAGCC
TGAACAGCCTGGCCTGCTGCTGGACCAACCAACGGCATCTCAATGAGCAGGGTGAG
ACCATCTTCATCCTGGGTGATGCTGGGTGGGCAAGTCCATGCTGCTACAGCGGTGCA
TAGCCTCTGGGCCACGGGCCGGCTAGACGCAGGGGTCAAATTCTTCTTCCACTTTCGCT
GCCGATGTTCACTGCTTCAAGGAAAGTGACAGGCTGTGTCTGCAGGACCTGCTCTTC
AAGCACTACTGCTACCCAGAGCGGGACCCGAGGAGGTGTTTGCCTTCTGCTGCGCTT
CCCCCAGGTGGCCCTCTTCACTTTCGATGGCCTGACAGAGCTGCACTCGGACTTGGACC
TGAGCCGCGTGCCTGACAGCTCTGCCCCCTGGGAGCCTGCCACCCCCCTGGTCTTGTG
GCCAACCTGCTCAGTGGGAAGCTGCTCAAGGGGGCTAGCAAGCTGCTCACAGCCCCGAC
AGGCATCGAGGTCCCGGCCAGTTCTGCGGAAGAAGGTGCTTCTCGGGGCTTCTCCC
TCAGCCACCTGCGGCCCTATGCCAGGAGGATGTTCCCGAGCGGGCCCTGCAGGACCGC
TTGCTGAGCCAGCTGGAGGCCAACCCCAACCTCTGCAGCCTGTGCTCTGTCCCCCTCTT
TTGCTGGATCATCTTCCGGTGTCTTCAGCACTTCCGTGCTGCTTGAAGGCTCACCAC
AGCTGCCCCACTGCACGATGACCCGACAGATGTCTTCTCTGCTGCTGAGGTCCAT
CTGAACAGGATGCAGCCCCAGCAGCCTGCTGCGAGCGGAACACACGAGCCCCAGTGGAGAC
CCTCCACGCGCGGCCGGGACACTCTGTGCTGCTGCGGAGGAGGTGCGCCACCGGGCATGG
AGAAGAGCCTCTTTGTCTTCAACCCAGGAGGAGGTGCAGGCCCTCCGGGCTGCAGGAGAGA
GACATGCAGCTGGGCTTCTGCGGGCTTTGCCGGAGCTGGGCCCCGGGGGTGACCAGCA
GTCTATAGATTTTTCCACCTCAGCCTCTCTCACCTGTAAACTGGGATCCAGTATAGA
CTTTGGAAATCAGTAGACACCATATGCTTCAAAAAACAGGGGCTATTAAATGACATCA
GGAGCCAGAAAGTCTCATGGCTGTGCTTCTCTTGAAGTTTATACAAACACAGATCA
CGATGTCGGAGCCAGAGTGGGAAAAACAAAAATAACAAGTGAAGGAGGAGATCTCG
CCCTGGCTGTGAAGAACAGCAATCAATCTCTGAGGTTGGGATGTGGGGCAATCAAGTT
GGGGATGAAGGAGCAAAAGCCTTCCAGAGGCTCTGCGGAACCAACCCAGCTTGACCAC
CCTGAGTCTTGCGTCCAACGGCATCTCCACAGAAGGAGGAAAGAGCCTTGCGAGGGCCC
TGCAGCAGAACAGTCTCTAGAAATACTGTGGCTGACCCAAAATGAACTCAACGATGAA
TTGGCAGAGAGTTTGGCAGAAATGTTGAAAGTCAACCAGAGCTTAAAGCATTTATGGCT
TATCCAGAAATCAGATCAGATCTTTTGTGTCAGTGTCTTAAAGGGGCTGCGCAGCGG
GACTATCAGGAGTCCACTGCCTCATGATGCAAGCCAGCTTCTGTGCAGAAGGTCTGG
TCGGCAAACTCCCTAAGTACCCGCTACAATTCTGCAGAAAAAGAATGTGTCTTGGAGC
TGTTGTAGTTACAGTAAATACACTGTGAAGAGACTTTATTGCCTATTATAATTATTTT
ATCTGAAGCTAGAGGAATAAAGCTGTGAGCAACAGAGGAGGCCAGCCTCACCTCATTC
CAACACCTGCCATAGGGACCAACGGGAGCGAGTTGGTCACCGCTCTTTTATTGAAGAG
TTGAGGATGTGGCACAAGTTGGTGCCAAAGCTTCTTGAATAAAACGTGTTTGATGGATT
AGTATTATACCTGAAATATTTTCTTCTCTCAGCACTTTCCCATGTATTGATACTGGT
CCCCTTTCAGAGCTGGAGACACCGGAGTATGTGCAGTGTGGGATTTGACTCCTCCAAGG
TTTTGTGGAAAGTTAATGTCAAGGAAAGGATGCACCACGGGCTTTTAAATTTAATCCTG
GAGTCTCACTGTCTGCTGGCAAAGATAGAGAATGCCCTCAGCTCTTAGCTGGTCTAAGA
ATGACGATGCCTTCAAAATGCTGCTTCCACTCAGGGCTTCTCCTCTGCTAGGCTACCTT
CCTCTAGAAGGCTGAGTACCATGGGCTACAGTGTCTGCGCTTGGGAAGAAGTATTCTG
CCCTTCAAAGAAATAGGGCATGGCTTGGCCCTGTGGCCCTGGCATCCAAATGGCTGCT
TTTGTCTCCCTTACCTCGTGAAGAGGGGAAGTCTCTTCTGCTTCCCAAGCAGCTGAAG
GGTGACTAAACGGGGCCCAAGACTCAGGGGATCGGCTGGGAAGTGGGCCAGCAGAGCAT
TTTGGACACCCCCACCATGGTGGGCTTGTGGTGGCTGCTCCATGAGGTTGGGGGTGAT
ACTACTAGATCACTTGTCTCTTGGCAGCTCATTTGTTAATAAAATACTGAAACACAA
AA
AAAAAAAAAAAAAA (SEQ ID NO:25)

FIG. 5

[illegible]

FIG. 6

Variable	Mean	Standard deviation	Minimum	Maximum
Age	34.5	10.5	20	55
Gender	0.5	0.5	0	1
Marital status	0.5	0.5	0	1
Education	12.5	1.5	10	15
Income	15.5	5.5	10	25
Health	0.5	0.5	0	1
Smoking	0.5	0.5	0	1
Alcohol	0.5	0.5	0	1
Exercise	0.5	0.5	0	1
Stress	0.5	0.5	0	1
Sleep	0.5	0.5	0	1
Appetite	0.5	0.5	0	1
Mood	0.5	0.5	0	1
Energy	0.5	0.5	0	1
Concentration	0.5	0.5	0	1
Memory	0.5	0.5	0	1
Emotion	0.5	0.5	0	1
Behavior	0.5	0.5	0	1
Thought	0.5	0.5	0	1
Feeling	0.5	0.5	0	1
Perception	0.5	0.5	0	1
Attention	0.5	0.5	0	1
Intuition	0.5	0.5	0	1
Imagination	0.5	0.5	0	1
Reasoning	0.5	0.5	0	1
Logic	0.5	0.5	0	1
Mathematics	0.5	0.5	0	1
Science	0.5	0.5	0	1
History	0.5	0.5	0	1
Geography	0.5	0.5	0	1
Language	0.5	0.5	0	1
Art	0.5	0.5	0	1
Music	0.5	0.5	0	1
Sports	0.5	0.5	0	1
Games	0.5	0.5	0	1
Reading	0.5	0.5	0	1
Writing	0.5	0.5	0	1
Speaking	0.5	0.5	0	1
Listening	0.5	0.5	0	1
Observing	0.5	0.5	0	1
Touching	0.5	0.5	0	1
Tasting	0.5	0.5	0	1
Smelling	0.5	0.5	0	1
Thinking	0.5	0.5	0	1
Feeling	0.5	0.5	0	1
Perceiving	0.5	0.5	0	1
Attending	0.5	0.5	0	1
Imagining	0.5	0.5	0	1
Reasoning	0.5	0.5	0	1
Logic	0.5	0.5	0	1
Mathematics	0.5	0.5	0	1
Science	0.5	0.5	0	1
History	0.5	0.5	0	1
Geography	0.5	0.5	0	1
Language	0.5	0.5	0	1
Art	0.5	0.5	0	1
Music	0.5	0.5	0	1
Sports	0.5	0.5	0	1
Games	0.5	0.5	0	1
Reading	0.5	0.5	0	1
Writing	0.5	0.5	0	1
Speaking	0.5	0.5	0	1
Listening	0.5	0.5	0	1
Observing	0.5	0.5	0	1
Touching	0.5	0.5	0	1
Tasting	0.5	0.5	0	1
Smelling	0.5	0.5	0	1
Thinking	0.5	0.5	0	1
Feeling	0.5	0.5	0	1
Perceiving	0.5	0.5	0	1
Attending	0.5	0.5	0	1
Imagining	0.5	0.5	0	1
Reasoning	0.5	0.5	0	1
Logic	0.5	0.5	0	1
Mathematics	0.5	0.5	0	1
Science	0.5	0.5	0	1
History	0.5	0.5	0	1
Geography	0.5	0.5	0	1
Language	0.5	0.5	0	1
Art	0.5	0.5	0	1
Music	0.5	0.5	0	1
Sports	0.5	0.5	0	1
Games	0.5	0.5	0	1
Reading	0.5	0.5	0	1
Writing	0.5	0.5	0	1
Speaking	0.5	0.5	0	1
Listening	0.5	0.5	0	

FIG. 7

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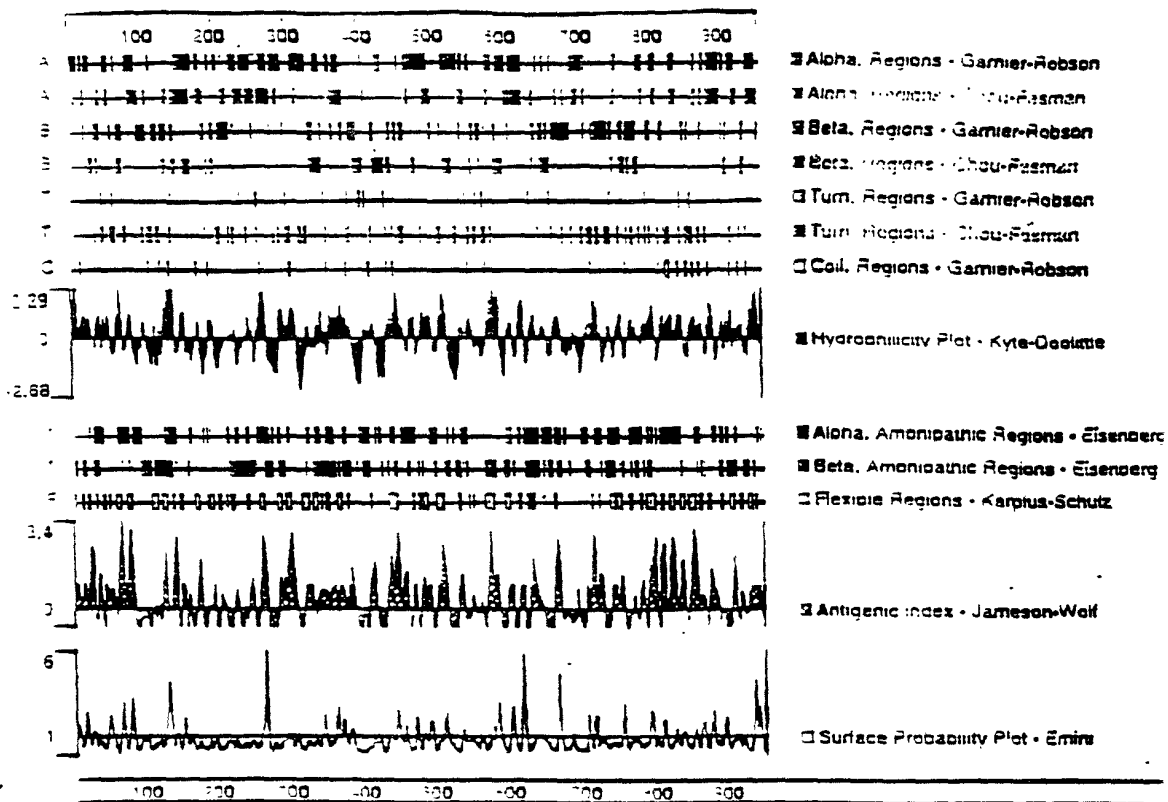


FIG. 8

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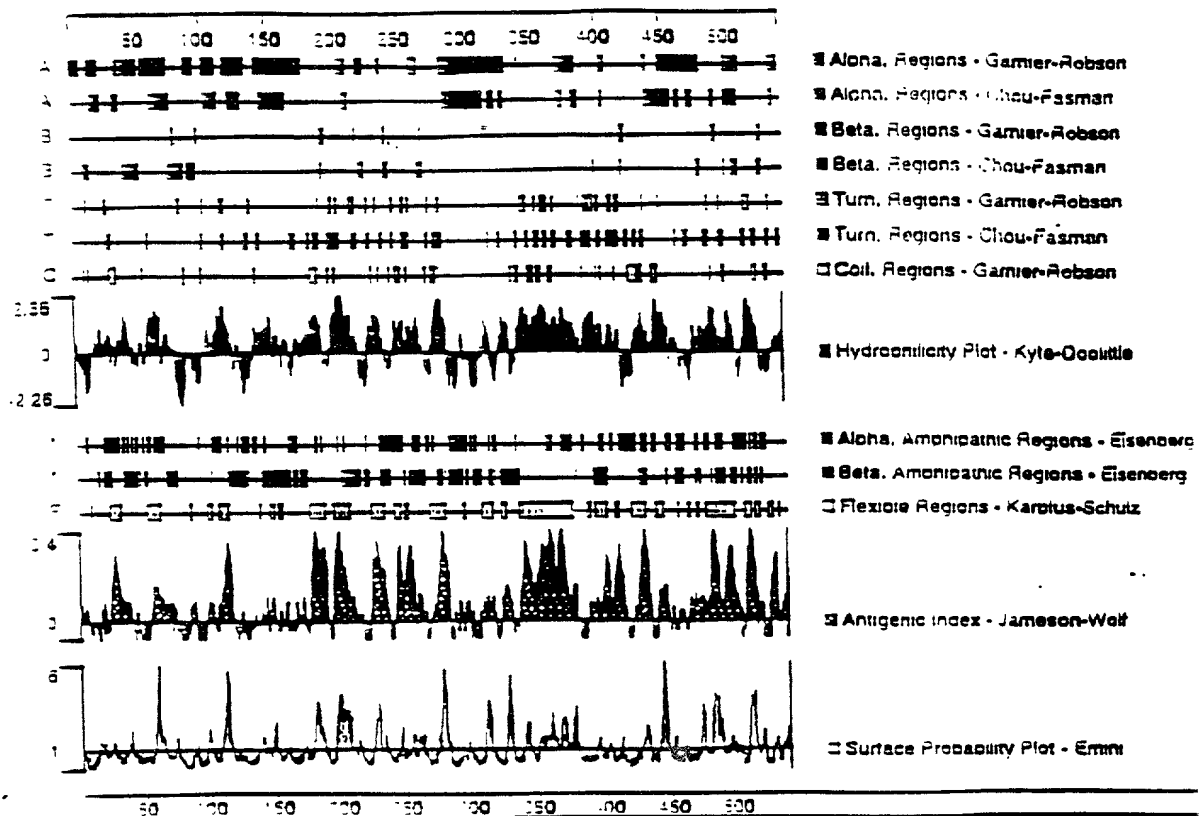


FIG. 9

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FIG. 10 (Page 1 of 3)

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CACGGCCCTTCTTTACAGCCTTCTTCTCTGCTGGACGACAGGGTGGGCACTCAGGAGCT
GCTCAGGTTCTTCCAGGAGTGGATGCCCCCTGCGGGGGCAGCGACCACGTCTCTGCTATCC
TCCCTTCTCTCCCGTTCCAGTGCCTGCAGGGCAGTGGTCCGGCGCGGGAAGACCTCTTCAA
GAACAAGGATCACTTCCAGTTCACCAACCTCTTCTCTGTGCGGGCTGTTGKCCAAAGCCAA
ACAGAAACTCTCTGCGGCATCTCGTGCCCGCGGCAGCCCTGAGGAGAAAGCGCAAGGCCCT
GTGGGCACACCTGTTTTTCCAGCCTGCGGGGGCTACCTGAAGAGCCTGCCCCGCGTTCAGGT
CGAAAGCTTCAACCAGGTGCAGGCCATGCCCACGTTTATCTGATGCTGCGCTGCATCTA
CGAGACACAGAGCCAGAAGGTGGGGCAGCTGGCGGGCCAGGGGCATCTGCGCCAACTACCT
CAAGCTGACCTACTGCAACGCCTGCTCGGCCGACTGCAGCGCCCTCTCTCTCGTCTTGCA
TCACTTCCCCAAGCGGCTGGCCCTAGACCTAGACAACAACAATCTCAACGACTACGGCGT
GCGGGAGCTGCAGCCCTGCTTCAGCCGCTCACTGTTCTCAGACTCAGCGTAAACCAGAT
CACTGACGGTGGGGTAAAGGTGCTAAGCGAAGAGCTGACCAAATACAAAATTGTGACCTA
TTTGGGTTTTATACAACAACCAGATCACCGATGTGCGAGCCAGGTACGTCAACAAAATCTCT
GGATGAATGCAAAGGCCTCACGCATCTTAACTGGGAAAAAACAAAATAACAAGTGAAGG
AGGGAAGTATCTCGCCCTGGCTGTGAAGAACAGCAAATCAATCTCTGAGGTTGGGATGTG
GGGCAATCAAGTTGGGGATGAAGGAGCAAAAGCCTTCGCAGAGGCTCTGCGGAACCACCC
CAGCTTGACCACCTGAGTCTTTCGTCCAACGGCATCTCCACAGAAGGAGGAAAGAGCCT
TGCGAGGGCCCTGCAGCAGAACACGTCTCTAGAAATACTGTGGCTGACCCAAAATGAACT
CAACGATGAAGTGGCAGAGAGTTTGGCAGAAATGTTGAAAGTCAACCAGACGTTAAAGCA
TTTATGGCTTATCCAGAATCASATCACAGCTWARGGGACTGCCCAGCTGGCAGATGCGTT
ACAGAGCAACACTGGCATAACAGAGATTTGCCTAAATGGAAACCTGATAAAACCAGAGGA
GGCCAAAGTCTATGAAGATGAGAAGCGGATTATCTGTTTTCTGAGAGGATGCTTTCTCTGTT
CATGGGGTTTTTGGCCCTGGAGCCTCAGCAGCAAATGCCACTYTGGGCAGTCTTTTGTGTC
AGTGTCTTAAAGGGGCCCTGCGCAGGCGGGACTATCAGGAGTCCACTGGCTCCATGATGCA
AGCCAGCTTCTCTGTGCAGAAGGTCTGGTGGGCAAACTCCCTAAGTACCCGCTACAATTCT
GCAGAAAAAGAATGTGTCTTGGCAGCTGTTGTAGTTACAGTAAATACACTGTGAAGAGAC
TTTATTGCCTATTATAATTATTTTTATCTGAAGCTAGAGGAATAAAGCTGTGAGCAAACA
GAGGAGGCCAGCCTCACCTCATTCCAACACCTGCCATAGGGACCAACGGGAGCGAGTTGG
TCACCGCTCTTTTCATTGAAGAGTTGAGGATGTGGCACAAGTTGGTGCCAAGCTTCTTG
AATAAAACGTGTTTGATGGATTAGTATTATACCTGAAATATTTTCTTCTCTCAGCACT
TTCCCATGTATTGATACTGGTCCCACTTCACAGCTGGAGACACCGGAGTATGTGCAGTGT
GGGATTTGACTCCTCCAAGGTTTTTGTGGAAAGTTAATGTCAAGGAAAGGATGCACCACGG

GCTTTTAATTTTAATCCTGGAGTCTCACTGTCTGCTGGCAAAGATAGAGAATGCCCTCAG
CTCTTAGCTGGTCTAAGAATGACGATGCCCTTCAAAATGCTGCTTCCACTCAGGGCTTCTC
CTCTGCTAGGCTACCCCTCCTCTAGAAGGCTCAGTACCATGGGCTACAGTGTCTGGCCTTG
GGAAGAAGTGATTCTGTCCCTCCAAAGAAATAGGGCATGGCTTGCCCCCTGTGGCCCTGGC
ATCCAAATGGCTGCTTTTGTCTCCCTTACCTCGTGAAGAGGGGAAGTCTCTTCCTGCCTC
CCAAGCAGCTGAAGGGTGACTAAACGGGCGCCAAGACTCAGGGGATCGGCTGGGAAGTGG
GCCAGCAGAGCATGTTGGACACCCCCCACCATGGTGGGCTTGTGGTGGCTGCTCCATGAG
GGTGGGGGTGATACTACTAGATCACTTGTCTCTTGCCAGCTCATTGTTAATAAAATAC
TGAAAACCCAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGG (SEQ ID NO:38)

FIG. 11

CACGCGTCCGCGCTACTSCGGGAGCAGCGTCCTCCCGGGCCACGGCGCTTCCCGGCCCGG
GCGTCCCGGACCATGGCGCTCTCCGGGCTCTTCTCTAGCTCTCAGCGGCTCGGAAGTCT
GTAAACCTGGTGGCCAGTGATTGTAAAGTCAGGAGACTTTCCTTCGGTTTTCTGCCTTTGA
TGGCAAGAGGTGGAGATTGTGGCGGCGATTACAGAAAAACATCTGGGAAGACAAGTTGCTG
TTTTTATGGGAATCGCAGGCTTGGGAAGAGACAGAAGCAATTCCAGAAATAAATTGGAAAT
TGAAGATTTAAACAATGTTGTTTTTAAAAATATTCTAACTTCAAAGAATGATGCCAGAACT
TAAAAAGGGGCTGCGCAGAGTAGCAGGGGGCCCTGGAGGGCGCGGCCTGAATCCTGATTGC
CCTTCTGCTGAGAGGACACACGCAGCTGAAGATGAATTTGGGAAAAGTAGCCGCTTGCTA
CTTTAACTATGGAAGAGCAGGGGCCACAGTGAGATGGAAATAATCCCATCAGAGTCTCACC
CCCACATTCAATTACTGAAAAGCAATCGGGAACCTTCTGGTCACTCACATCCGCAATACTC
AGTGTCTGGTGGACAACCTTGCTGAAGAATGACTACTTCTCGGCCGAAGATGCGGAGATTG
TGTGTGCCTGCCCCACCCAGCCTGACAAGGTCCSCAAAATTCTGGACCTSGTACAGAGCA
AGGGCGAGGAGGTGTCCGAGTTCTTCTCTACTTGTCTCCAGCAACTCGCAGATGCCTACG
TGGACCTCAGGCCTTGGCTGCTGGAGATCGGCTTCTCCCCCTTCCCTGCTCACTCAGAGCA
AAGTCGTGGTCAACACTGACCCAGGTAGGAGTCAGCCCCAGCAAGACCGCAGGCACCAGT
GCAAGCAGGGCCCTGGGGGTTTTGGTAATGGCTGGGCCAGCCCTGAGTGCCACCTCAGGA
AGCAGGGCCCAGGTGCTATTTTGATTTTAGAAAAGGAACAGCTGAATCCTGTCTCCCAAGTG
CAGCCCAGGTGGCTGCGATTGAACTSCCCACACCTCGATGGTCTGGTTTTATAGAGGGGCC
TTTGGAAGTATGGGAATGGCCTGTGTTCTGACCCCTTGCTTTCTTCTTCTTCTGACATAT
GTAGACATTTTAAATGGTTGCACAAATCAAGGTTGTATTTTTTTTTCTTTAAAAAAATCT
TTAGCTGGACATGGTAGCACACACCTGTAGTTCCAGCTACTCAGGAGGCTGAGGCAAGAG
GACTGCTTGAGCCCCAGAGTCTAAGGCTGCAGCGAGCTATGATTGTGCCCTACACTCCA
CAGCCTGGGTTTTAGAGTGAGACCCTGTCTCTAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAANGGGCGG (SEQ ID NO:40)

FIG. 12

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MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCLVDNLLKNDYFSAEDAETVCA
CPTQPBKVRKILDLVQSKGEEVSEFFLYLLQQLADAYVDLRPWLLLEIGFSPSLLTQSKV
VNTDPGRSQPQQDRRHQCKQGFGGNGWASPECHLRKQAQVLF
(SEQ ID NO:41)

FIG. 13

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	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2433	2434	2435	2436	2437	2438	2439	2440	2441	2442	2
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[illegible]

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-----TXXKXKXKXKX-----Majority			
	330	340	350 360
112	-----T T A T Q S S T P R-----		
141	-----T T A T Q S S T P R-----		
161	-----T T A T Q S S T P R-----		
	-----P C-----Majority		
	370	380	390 400
112	-----R C-----		
141	-----R C-----		
161	-----R C-----		
	-----L P X C-----Majority		
	410	420	430 440
124	-----L P S C-----		
141	-----L P S C-----		
161	-----L P S C-----		
	-----Majority		
	450	460	470 480
128	-----		
141	-----		
161	-----		
	-----G P G G-----Majority		
	490	500	510 520
128	-----		
141	-----G P G G-----		
161	-----G P G G-----		
	-----F X X K X K X K X-----Majority		
	530	540	550 560
128	-----C A S-----		
141	-----C A S-----		
161	-----C A S-----		
	-----Majority		
	570	580	590 600
131	-----P-----		
153	-----P-----		
161	-----P-----		
	-----X W X-----Majority		
	610	620	630 640
112	-----T W P-----		
153	-----T W P-----		
161	-----T W P-----		

FIGURE 14 (2 of 4)

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-----XKPKKKV-----				Majority
	650	660	670	680
148	-----SSPSMAW-----			CARD4-Y CLONE
153	-----SSPSMAW-----			CARD4-Z CLONE
641	ISFNQVQAMPTFTWMLRCITETQSQKVGQLAARGICANYL			CARD4L
-----XCKKXX-----				Majority
	690	700	710	720
148	-----TSCTRT-----			CARD4-Y CLONE
153	-----TSCTRT-----			CARD4-Z CLONE
651	ALTVCNACGSADCSALSFVLHHFPRRLALDLDNNNLNDYGV			CARD4L
-----				Majority
	730	740	750	760
148	-----			CARD4-Y CLONE
153	-----			CARD4-Z CLONE
711	FELQPCFSRLTVLRLSVNQITDGGVXVLSSELTXYKIIVTY			CARD4L
-----ECK-----				Majority
	770	780	790	800
148	-----			CARD4-Y CLONE
153	-----			CARD4-Z CLONE
761	LGLYNNQITDVGARYVTKILD ECKGLTHLSLYNNQITDVG			CARD4L
-----WXXXXXXXXXX-----				Majority
	810	820	830	840
148	-----			CARD4-Y CLONE
155	-----			CARD4-Z CLONE
801	ARLGKNKITSEGGKYLALAVKNSKSSISEVGMWGNQVGDEG			CARD4L
XXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX				Majority
	850	860	870	880
149	-----			CARD4-Y CLONE
155	-----LRKQA-----			CARD4-Z CLONE
841	AKAFAEA LRPNHPSLTTL SLASNGISTEGGKSLARALQQNT			CARD4L
XX				Majority
	890	900	910	920
149	-----			CARD4-Y CLONE
161	---QVL-----			CARD4-Z CLONE
931	SLLELWLTQNELNDEVAESLAEMLKVNQTLKHLWLIQNQI			CARD4L
XX				Majority
	930	940	950	960
149	-----			CARD4-Y CLONE
164	-----			CARD4-Z CLONE
951	TAKSTAGLADALQSNTTETETICLNGNLKPEEAKVYEDEK			CARD4L

FIGURE 14 (3 of 4)

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<u>XXXXF</u>				Majority
149				CARD4-Y CLONE
154	-	-	- F	CARD4-Z CLONE
161	F	-	- C F	CARD4L
Decorations: Decoration #1: Shade (in solid black) residues that match the Consensus exactly.				

149 154 161

CCACGCGTCCGCGGACCCCGAGCGGTAGCGCCCTCCCTCCCAGCTGTTGTCCCGCCCGAT
CCGCGACCCCTAGTCCCGCGATCCCGCTTGTGAGAGTCACCGTACTCCAGGGCCAACTGAG
CCAAAGTCCTGCCAACTTGGGTGAGCAATGAAAGGCAGGATCCTGGGTGGTGGCCCTGAA
TCCTGATTTGTCTGCCCTGCCAGCGAGACACATGTGGTCAAAGATGAATTTGAGAAAAGT
AGCTGCTGGCTACTTGAACAATGGAGGAACACGGCCATCATGAGATGGAAGGCACCCCAT
TGGGTTGTCACTCCACATTAAGTCTGTAAGATCAACAGGGAACATCTGGTCACCAACA
TTCGGAACACTCAGTGTCTGGTGCACAACTTGGCTGGAGAATGGCTACTTCTCAGCCGAAG
ATGCAGAGATTGTGTGTGCCTGTCCCAACCAAGCCTGACAAGGTCCGAAAGATCCTTGACC
TGGTGCAGAGCAAAGGCGAGGAGGTGTCTGAGTTCTTCCTCTACGTGCTGCAGCAGCTGG
AGGATGCTTACGTGGACCTCAGGCTGTGGCTCTCAGAAATTGGCTTCTCCCGTTCCCGAGC
TCATTCCGACCAAACCTATCCTCAATACTGACCCAGTAAGCAGGTATACCCAACAGCTGC
GACACCAACTGGGCCCGACTCCAAGTTCATGCTGTGCTACGCCCAGAAGGAGGACCTGC
TGCTGGAGGAGACCTATATGGACACACTCATGGGGCTGGTAGGCTTCAACAATGAAAACC
TGGGCAGCCTAGGAGGCCTGATTGCCCTGCTGGACCACAGTACGGGCGTCTCAACGAGC
ATGGCGAGACTGTCTTCGTGTTCGGGGACGCGGGAGTGGGCAAGTCCATGCTGCTGCAGA
GGTTGCAGAGCCTCTGGGCGTCAGGCAGGTTGACCTCCACAGCCAAATTCTTCTTCCACT
TCCGCTGCCGATGTTTCAGCTGCTTCAAGGAGAGCGACATGCTGAGTCTGCAGGACCTGC
TCTTCAAGCATTTCTGCTACCCGGAGCAGGACCCCGAGGAGGTGTTCTCCTTCTTGCTGC
GCTTTCCCCACACAGCGCTCTTCACTTTTGACGGCCTGGATGAGCTGCACTCAGACTTCG
ACCTGAGCCGCGTGCCGGATAGCTGCTGCCCTGGGAGCCGGCTCACCTCTGGTCTGCTGC
TGGCTAACCTCCTAAGTGGGAGGCTGCTCAAGGGTGCCGGCAAATTGCTCACTGCTCGCA
CAGGCGTGGAGGTCCCCCGCCAGCTCCTGCGCAAAAAGGTGCTGCTCCGGGGCTTCTCCC
CAAGTCACCTGCGCGCCTATGCCCGCCGATGTTCCCCGAGCGCACAGCGCAGGAGCATC
TGCTGCAGCAGCTGGATGCCAACCCCAACCTCTGCAGCCTGTGCGGGGTGCCGCTCTTCT
GTTGGATCATCTTCCGTTGTTTCCAGCACTTCCAGACGGTCTTCGAGGGCTCCTCTTCAC
AGTTGCCCGACTGTGCTGTGACCCTGACCGATGTCTTTCTGCTGGTCACTGAGGTGCATC
TGAACAGGCCCGCAGCCAGCAGCCTGGTGCAGCGCAACACGCGCAGCCCGCGGAAACCC
TACGTGCAGGCTGGCGCACGCTGCATGCGCTGGGAGAGGTGGCTCACCGAGGCACCGACA
AGAGCCTCTTTGTGTTTGGCCAGGAGGAGGTGCAGGCGTCCAAGCTGCAGGAAGGAGATC
TGCAGCTGGGCTTCTGCGGGCTTTGCCCGATGTGGGCCCTGAGCAGGGCCAGTCTTACG
AATTTTCCACCTTACGCTCCAGGCCTTCTTCAACCGCTTCTTCTGCTAGCAGATGACA
AAGTCAGCACCCGGGAGTTGCTGAGGTTCTTTGAGAATGGACGTCTCCTGGAGAGGCAA

FIG. 15 (Page 1 of 3)

097234.40400

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CAAGCTCGTCCTGCCATTCTTCCTTCCTTCCTTCCTTCAGTGCCTGGGCGGCAGAAAGCCGGT
TGGGCCCTGATCCTTTTCAGGAACAAAGATCACTTCCAGTTCACCAACCTCTTCGTGTGCG
GGCTACTGGCCAAAGCCCCACAGAACTCCTTCGGCAGCTGGTGGCCAAAGGCTATCCTGA
GGAGGAAGCGCAAGGCCCTGTGGGCTCACCTGTTTGCTAGCCTGCGCTCCTACTTGAAGA
GCCTACCTCGGGTCCAGTCTGAGGCTTTAACCAGGTGCATGCCATGCCACATTCTGT
GGATGCTGCGCTGCATCTATGAGACGCAGAGCCAGAAGGTGGGGCGCCTCGCCGCCAGGG
GCATCAGTGGGACTACCTCAAGCTGGCCTTTTGCAACGCTTGCTCTGCGGACTGCAGCG
CCCTGTCTCTTCGTCTCTGCATCACTTCCACAGGCAGCTGGCCCTAGACCTGGACAACAACA
ACCTCAATGACTATGGCGTGCAGGAGCTGCAGCCTTGCTTTAGCCGTCTCACGGTTATCA
GACTCAGCGTCAACCAGATCACCGACACGGGGGTGAAGGTGCTATGTGAGGAACTGACCA
AGTATAAGATCGTGACGTTCTCGGTTTATACAACAACCAGATAACTGATATCGGAGCCA
GGTATGTGGCCCCAATCCTGATGAATGCAGAGGCCTCAAGCACCTTAAACTAGGGAAAA
ACAGAATAACAAGTGAGGGCGGGAAGTGTGTGGCTTTGGCTGTGAAGAACAGCACCTCCA
TCGTTGATGTTGGGATGTGGGGTAATCAGATTGAGACCAAGGGGCAAAGGCCCTTCGCAG
AGGCATTGAAGGACCACCCAGCCTGACCACTCTCAGTCTTGCAATTCAATGGCATCTCTC
CGGAGGGAGGGAAGAGCCTTGCGCAGGCCCCGAAGCAGAACACCACACTGACAGTAATCT
GGCTGACCAAAAATGAACTTAATGATGAGTCTGCAGAGTGCTTCGCTGAGATGCTGAGAG
TGAACCAGACGCTACGGCATTATGGCTGATCCAGAATCGCATCACAGCCAAGGGGACAG
CGCAGCTGGCGAGGGCACTGCAGAAGAACACAGCCATAACAGAGATTTGTCTCAATGGAA
ACTTGATTAAGCCCCAGGAGGCCAAAGTCTTCGAGAATGAGAAGAGAATCATCTGCTTCT
GACGGACGCTCCTGGGCAGGATCTTTGTCTAGGTTGCTCCTCAGTCACAGACAGCACTG
TGCAGTCAGCAGGGTAGCAGGATGCTGTGCAGCGCCTGCAGCAAGGTGCCTGTGAGGAGC
CCACACCTCCACAGTGCACACCCATGTCCCTGCTCATGCTTGGACTGGTAGCACCCGCG
CCGCGGCTGAGACCCTGCAGACCGAGGGAGTCTTAGGAACCATCGTCACTCAAGGCC
AGCAGGGCATCTTCTGTACAAAGATCTCCCTGCATATCCACTAGACGGAAGCTGAAGGAA
CGCAACAGCAGAGGAGGCCAACAGACGCCTGGCTGAAGGCTCCGTGGGACCAACGGTGTG
ACCTTCAGAAAAGAGCTGGGAACTTGAGCAGAGCCGATGGTAACTTCTTGGGGAAAGAAG
GCACCCAGTGACTGCATGGTTATTCTGAGTCTCCTTCCTCTGCTTAGTCCCTCTCACTG
TACAGGTCTGTTTCTTCCTCGCAGCTGTGGCTGCTGAAGTAGGTCCACTGTGGGGAGAGC
TCATCACAGACTTTGGTTCGGTTCTGATTCTCAGTGGTGGCAACCGAGAGTCAGACGAT
ACCTCTAGGTGAGTCTCAGAGGATCTCTATGCTGTGAGAGGGTTGAGGGCCACCCAGA
ATTTTTTTTTTTTACCAGTTTTTACTGTGCCTGCCCCAGGAGGGAGAATTACTTCCAGC

FIG. 15 (Page 2 of 3)

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CTCCACAGCAGCAGGCATGGCTTSCCTCAATGGTCCTGAGATCCCAACAAAACCTCTCTCC
CTTGCCTGTGAGCAGAAAGTATCTTCATGTCTCAGAAGTTGGAGGGTGACTGGACACAG
TTAAGACTCAGAGAGCCAGCTGATAGCTCAAAGCAAAGCATGGCACATACCCACCACCAT
ACCATGGTGCGCATGGGATGGGACAGTTGGAATGTTGCAGATAACGTGTTCTTTTGCCAG
TTCATTTGTTAATAAAATATTTAAACGTTAAAAAAAAAAAAAAAAAAAAAAAAAGGGCG
G (SEQ ID NO:42)

FIG. 13 (Page 3 of 3)

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FIG. 16

	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2433	2434	2435	2436	2437	2438	2439	2440	2441	2442	2
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FIGURE 17

Variable	Mean	SD	Min	Max	Skewness	Kurtosis	Normality
Age	35.2	12.5	18	65	0.15	3.2	0.98
Gender	0.52	0.50	0	1	-0.02	3.0	0.99
Marital Status	0.68	0.47	0	1	0.10	3.1	0.99
Education	12.5	2.1	9	16	-0.10	3.3	0.98
Income	15.2	8.5	5	35	0.20	3.4	0.97
Occupation	1.2	0.8	0	2	-0.05	3.0	0.99
Religion	1.5	0.5	1	3	-0.10	3.1	0.99
Health Status	1.8	0.4	1	3	-0.05	3.0	0.99
Stress Level	2.5	1.2	1	4	0.15	3.2	0.98
Life Satisfaction	3.2	1.5	1	5	-0.10	3.3	0.98
Resilience	2.8	1.0	1	4	-0.05	3.0	0.99
Optimism	3.5	1.2	1	5	-0.10	3.3	0.98
Gratitude	3.8	1.0	1	5	-0.05	3.0	0.99
Forgiveness	3.6	1.1	1	5	-0.10	3.3	0.98
Empathy	3.4	1.0	1	5	-0.05	3.0	0.99
Self-Compassion	3.7	1.1	1	5	-0.10	3.3	0.98
Emotional Regulation	3.9	1.0	1	5	-0.05	3.0	0.99
Psychological Well-being	4.1	1.2	1	5	-0.10	3.3	0.98
Life Purpose	4.0	1.1	1	5	-0.05	3.0	0.99
Meaning in Life	4.2	1.0	1	5	-0.05	3.0	0.99
Existential Well-being	4.3	1.1	1	5	-0.10	3.3	0.98
Transcendental Well-being	4.4	1.0	1	5	-0.05	3.0	0.99
Humanistic Well-being	4.5	1.1	1	5	-0.10	3.3	0.98
Existential Well-being	4.6	1.0	1	5	-0.05	3.0	0.99
Transcendental Well-being	4.7	1.1	1	5	-0.10	3.3	0.98
Humanistic Well-being	4.8	1.0	1	5	-0.05	3.0	0.99
Existential Well-being	4.9	1.1	1	5	-0.10	3.3	0.98
Transcendental Well-being	5.0	1.0	1	5	-0.05	3.0	0.99
Humanistic Well-being	5.1	1.1	1	5	-0.10	3.3	0.98
Existential Well-being	5.2	1.0	1	5	-0.05	3.0	0.99
Transcendental Well-being	5.3	1.1	1	5	-0.10	3.3	0.98
Humanistic Well-being	5.4	1.0	1	5	-0.05	3.0	0.99
Existential Well-being	5.5	1.1	1	5	-0.10	3.3	0.98
Transcendental Well-being	5.6	1.0	1	5	-0.05	3.0	0.99
Humanistic Well-being	5.7	1.1	1	5	-0.10	3.3	0.98
Existential Well-being	5.8	1.0	1	5	-0.05	3.0	0.99
Transcendental Well-being	5.9	1.1	1	5	-0.10	3.3	0.98
Humanistic Well-being	6.0	1.0	1	5	-0.05	3.0	0.99
Existential Well-being	6.1	1.1	1	5	-0.10	3.3	0.98
Transcendental Well-being	6.2	1.0	1	5	-0.05	3.0	0.99
Humanistic Well-being	6.3	1.1	1	5	-0.10	3.3	0.98
Existential Well-being	6.4	1.0	1	5	-0.05	3.0	0.99
Transcendental Well-being	6.5	1.1	1	5	-0.10	3.3	0.98
Humanistic Well-being	6.6	1.0	1	5	-0.05	3.0	0.99
Existential Well-being	6.7	1.1	1	5	-0.10	3.3	0.98
Transcendental Well-being	6.8	1.0	1	5	-0.05	3.0	0.99
Humanistic Well-being	6.9	1.1	1	5	-0.10	3.3	0.98
Existential Well-being	7.0	1.0	1	5	-0.05	3.0	0.99
Transcendental Well-being	7.1	1.1	1	5	-0.10	3.3	0.98
Humanistic Well-being	7.2	1.0	1	5	-0.05	3.0	0.99
Existential Well-being	7.3	1.1	1	5	-0.10	3.3	0.98
Transcendental Well-being	7.4	1.0					

FIG. 18 (1 of 10)

tgtatgattctgtttatatgaaatgtccagaaaaggtaaactctatagacaaaagcaaatcagtagt
 tgcctacggcccagggtattggctacaaataggctccagaaaactctgggaagatggtagagatgt
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FIG. 18 (3 of 10)

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FIG. 18 (6 of 10)

FIG. 18 (7 of 10)

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gttctgggagcctccagagcatgctcctctgtgtgtgacttcatgggactgggctctgagaaggc
tgtggctttgttggccctgccagggactgccacaccaggccacagggttgtgggtgagctggccg
gggagccacgttcaggggagcagctctgcttggagccaacacttacagagtaagccttctccttgg
acttgttaactgtactgacacttatttctacctcattcctttctgaaaaataacttggaaagtctga
agtcccttgatgagttctgtctttaagaacagaaaattagaggtgaacaatgaacactgtaaatta
cagaaaatgtatcccactccagtataacagcttctgtgaggctatctcctccagactgtggctct
gggagggtggggcctgagtcaaggctcctagggactagtgtgtgtcttcaatttattccttgaata
acgaaaacgcttgagcatcagggactgtgctagcaccacaaaatccagtggtgaacaacatggcttc
atgggttactgtctagaaaagggaagcacattaaagaaaaaatcatttgcgtaattatttaaat
tacaactgtgatgggtactatcacaaaggggaaggccaagaggggaacctgatttagatgaggttg
cagggaaggcctctctgaggaagcagcacttacactaagccatgaaggatgaataggagctagtc
agctgaggtgagttattctgcgtagggaacagcatgtgcaaaagggtctggggcaggagggagtggtg
gtgtcctggaagaactgccagaagctgctgtgccccagggttcagacagtggtggaagaggggact
acaggaggctgaggagataggcagggactggaccataaaagatctgtgggtcatgatgtgcattt
tggcttttatcctaaaagtgtatggaaagttagtgaacagtttgaagcaggagagggcatgtgatca
gatctgcaatgcaaaaagaccaattcttggctcttctaggaaactgaattggagaaggccagagc
acgtggaaatgacctgtcagtaggacattgtactgatgcagggaagagatgatgggtgctcagac
caagatggccggccaaagacatagaggttccaggggaggcattcttaggaattaggggga
gaactttgtgatacaaggaacatggggatgagaaggaagggtgtccaggttgacccccagggttact
aacctgctcagcaggatgagagtggtccattcactaagccaggggaccctaggaggtgtggctac
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ctcagatgtagaggtcacatggaggagaatataggaaaggaaattgaagttagagtgctcagatgc
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gaggtcaggacagccaaaatcctgaggggccaagaaagacaagacctggaaaatgtcattaaattc
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gatccatgctaataatgaaggaactatctgcaaaagggtatgttcccttaatttcaggggatacatgtg

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tattgtgtgatacacgagtgtgtgctatgaacacaccttgggaaggagtggtgcgaggatccttaa
cattttacctgtgtacttttgtcttctctcttttcaacagcctaaatggaaacctgataaaacca
gaggaggccaaagtctatgaagatgagaagcggattatctgtttctgagaggatgctttcctgtt
catgggggtttttgccctggagcctcagcagcaaatgccactctgggcagtcttttgtgtcagtgt
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gtcttgcgagctgtttagttacagtaaatacactgtgaagagactttattgcctattataa

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1 GTGACCCACCGCTCCGGCAGCAGGCAGGCTGCAGCAGGCGAGCAGCAGCAAGAGTAAAGG
CAGCTGGGTGCGCAGGCCGTCCGTCCGACGTCGTCGCTCGTTCATTTTC

63 TGACCGCGGCTGCCCCACCCAGAGCCATGGGGCGGGCAGAGATGCCATCCTGGACGCTCTT
ACTGGCGCCGACGGGTGGGGTCCGTACCCCGCCCGTGTCTACGGTAGGACCTGCGAGAA
1 M G R A R D A I L D A L

125 GAAAACTTGTTCAGGGGATGAACTCAAAAAGTTCAAGATGAAGCTGCTGACAGTGCAACTGCG
CTTTTGAACAGTCCCTACTTGAAGTTTTCAGTTCTACTTCGACGACTGTTCAGTTGACGC
13 E N L S G D E L K K F K M K L L T V Q L R

187 AGAAGGCTATGGGCGCATCCACGCGGGGCCCTGCTGCAGATGGACGCCATAGATCTCACTG
TCTTCCGATACCCGCTAGGGTCCGCCCGGGACGACGCTACCTGCGGTATCTAGAGTGAC
33 E G Y G R I P R G A L L Q M D A I D L T

249 ACAAACCTTGTTCAGTACTATCTGGAGTCTGATGGCTTGGAGCTCACAATGACTGTGCTTAGA
TGTTTGAACAGTTCGATGATAGACCTCAGCATAACCAACCTCGAGTGTACTGACACGAATCT
54 D K L V S Y Y L E S Y G L E L T M T V L R

311 GACATGGGCTTACAGGAGCTGGCTGAGCAGCTGCAAACGACTAAAGAAGAGTCTGGAGCTGT
CTGTACCCGAATGTCTCGACCGACTCGTCGACGTTTGTCTGATTTCTTCTCAGACCTCGACA
75 D M G L Q E L A E Q L Q T T K E E S G A V

373 GGCAGCTGCAGCCAGTGTCCCTGCTCAGAGTACAGCCAGAACAGGACACTTTTGTGGACCAGC
CCGTCCGACGTCGGTCACAGGGACGAGTCTCATGTCCGTCTGTCTCTGTGAAACACCTGGTCG
95 A A A A S V P A Q S T A R T G H F V D Q

435 ACAGGCAAGCACTCATTGCCAGGGTCACAGAAGTGGACGGAGTGTCTGGATGCTTTGCATGGC
TGTCGGTTTCGTGAGTAACGGTCCAGTGTCTTCACTGCCTCAGGACCTACGAAACGTACCG
116 H R Q A L I A R V T E V D G V L D A L H G

497 AGTGTGCTGACTGAAGGACAGTACCAGGCAGTTGCTGCAGAGACCACCAGCCAAGACAAGAT
TCACACGACTGACTTCCCTGTCTCGTCCGTCAAGCACGTCCTCGGTGGTCCGGTTCTGTTCTA
137 S V L T E G Q Y Q A V R A E T T S Q D K M

559 GAGGAAGCTCTTCAGCTTTGTTCCATCCTGGAACCTGACCTGCAAGGACTCCCTCCTCCAGG
CTCCTTCGAGAAGTCAAAACAAGTAGGACCTTGGACTGGACGTTCTTGAGGAGGAGGTCC
157 R K L F S F V P S W N L T C K D S L L Q

621 CCTTGAAGGAAATACATCCCTACTTGGTGATGGACCTGGAGCAGAGCTGAGGTATCTTTTCC
GGAACCTTCCCTTATGTAGGGATGAACCACTACCTGGACCTCGTCTCGACTCCATAGAAAAGG
178 A L K E I H P Y L V M D L E Q S

683 AGCTACATTATCTAGCTCCTGACTTTGTATACACAATTTTGAACCAATTTGTATTGT
TCGATGTAATAGATCGAGGACTGAAACATATGTGTTAAACCTTTTGTAAACATAAACA

745 GTTTAAAAAAAAAAAAAAAAAAGGGCGGCCGC
CAAAATTTTTCCTCCCGCGCG

1 CGCGTCGGCTGCAGCGGGGTGAGCGGGCGCAGCGGGCGGGGATCCTGGAGCCATGGGGC
GCGCAGGCGGACGTGCGCCCACTGCGCCCGCTGCGCGGCCCTAGGACCTCGGTACCCCG
1► M G

61 GCGCGCGGACGCCATCCTGGATGCGCTGGAGAACCTGACCGCCGAGGAGCTCAAGAAGT
CGCGCGCGCTGCGGTAGGACCTACGCGACCTCTTGGACTGGCGGCTCCTCGAGTTCTTCA
3► R A R D A I L D A L E N L T A E E L K K

121 TCAAGCTGAAGCTGCTGTCGGTGCCGCTGCGCGAGGGCTACGGGCGCATCCCGCGGGGCG
AGTTCCGACTTCGACGACAGCCACGGCGACGCGCTCCCGATGCCCGCTAGGGCGCCCCGC
23► F K L K L L S V P L R E G Y G R I P R G

181 CGCTGCTGTCCATGGACGCCCTTGGACCTCACCGACAAGCTGGTCAGCTTCTACCTGGAGA
GCGACGACAGGTACCTGCGGAACCTGGAGTGGCTGTTGACCACTCGAAGATGGACCTCT
43► A L L S M D A L D L T D K L V S F Y L E

241 CCTACGGCGCCGAGCTCACCGCTAACGTGCTGCGCGACATGGGCCTGCAGGAGATGGCGG
GGATGCCGCGGCTCGAGTGGCGATTGCACGACGCGCTGTACCCGAGCTCCTCTACCCGG
63► T Y G A E L T A N V L R D M G L Q E M A

301 GGCAGCTGCAGGCGGCCACGCACAGGGCTCTGGAGCCGCGCCAGCTGGGATCCAGGCCC
CCGTGCGACGTCCGCGGCTGCGTGGTCCCGAGACCTCGGCGCGGTGACCCCTAGGTCCGGG
83► G Q L Q A A T H Q G S G A A P A G I Q A

361 CTCCTCAGTCGGCAGCCAAGCCAGGCCTGCACTTTATAGACCAGCACCGGGCTGCGCTTA
GAGGAGTCAGCCGTGCGTTCCGTCGCGACGTGAAATATCTGGTCTGGCCCCGACGCGAAT
103► P P Q S A A K P G L H F I D Q H R A A L

421 TCCTGAGGGTCACAAACGTTGAGTGGCTGCTGGATGCTCTGTACGGGAAGGTCTTGACGG
AGCGCTCCCACTGTTGCAACTCACCGACGACCTACGAGACATGCCCTTCCAGGACTGCC
123► I A R V T N V E W L L D A L Y G K V L T

481 ATGAGCAGTACCAGGCAGTGCGGGCCGAGCCACCAACCCAAGCAAGATGCGGAAGCTCT
TACTCGTCATGGTCCGTACGCCCCGGCTCGGGTGGTTGGGTTCGTTCTACGCCCTTCGAGA
143► D E Q Y Q A V R A E P T N P S K M R K L

541 TCAGTTTCACACCAGCCTGGAACCTGACCTGCAAGGACTTGCTCCTCCAGGCCCTAAGGG
AGTCAAAGTGTGGTCCGACCTTGACCTGGACGTTCTGAAACGAGGAGTCCGGGATTCCTC
163► F S F T P A W N W T C K D L L L Q A L R

601 AGTCCCAGTCCTACCTGGTGGAGGACCTGGAGCGGAGCTGAGGCTCCTTCCAGCAACAC
TCAGGGTCAGGATGGACCACTCCTGGACCTCGCCTCGACTCCGAGGAAGGGTCGTTGTG
183► E S Q S Y L V E D L E R S

661 TCCGGTCAGCCCCCTGGCAATCCACCAATCATCCTGAATCTGATCTTTTATACACAAT
AGGCCAGTCGGGGACCGTTAGGGTGGTTTAGTAGGACTTAGACTAGAAAAATATGTGTTA

721 ATACGAAAAGCCAGCTTGAA
TATGCTTTTCGGTCGAACCTT

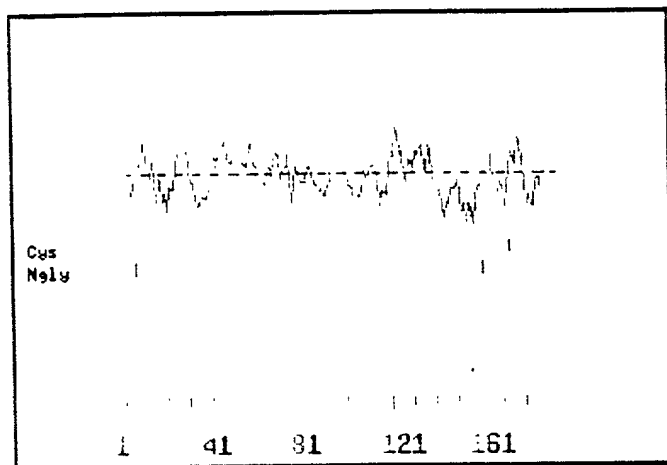


FIG. 22

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ALIGN calculates a global alignment of two sequences
 version 2.0u Please cite: Myers and Miller, CABIOS (1989)
 > hCARD5-DNA 740 aa vs.
 > mCARD5-DNA 763 aa
 scoring matrix: paml20.mat, gap penalties: -12/-4
 68.2% identity; Global alignment score: 2377

```

      10      20      30
inputs C---GCGTCCGGCTGCAG-CGGGGTG-----AGCG-GCGGCAGC-----GGC
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
      CCACGCGTCCGGCAGCAGGCTGCAGCAGGCGAGCAGCAGCAAGAGTAAAGGTGAC
      10      20      30      40      50      60

      40      50      60      70      80      90
inputs CGGGGAT-----CCTGGAGCCATGGGGCGCGCGCGACGCCATCCTGGATGCGCTGGA
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
      CGCGGCTGCCCCACCCAGAGCCATGGGGCGGGCAGAGATGCCATCCTGGACGCTCTTGA
      70      80      90      100     110     120

      100     110     120     130     140     150
inputs GAACCTGACCGCCGAGGAGCTCAAGAAGTTCAAGCTGAAGCTGCTGCGGTGCCGCTGCG
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
      AAACCTTGTCAGGGGATGAACTCAAAAAGTTCAAGATGAAGCTGCTGACAGTGCAACTGCG
      130     140     150     160     170     180

      160     170     180     190     200     210
inputs CGAGGGGTACGGGCGCATCCCGCGGGGCGCGCTGCTGTCCATGGACGCCTTGGACCTCAC
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
      AGAAGGCTATGGGCGCATCCACGCGGGGCCCTGCTGCAGATGGACGCCATAGATCTCAC
      190     200     210     220     230     240

      220     230     240     250     260     270
inputs CGACAAGCTGGTCAGCTTCTACCTGGAGACCTACGGCGCCGAGCTCACCCTAAC-GTGC
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
      TGACAAACTTGTCAGCTACTATCTGGAGTCGTATGGCTTGGAGCTCAC-AATGACTGTGC
      250     260     270     280     290

      280     290     300     310     320     330
inputs TGCGCGACATGGGCCTGCAGGAGATGGCCGGGCAGCTGCAGGCGGCCACGCACCGGGCT
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
      TTAGAGACATGGGCTTACAGGAGCTGGCTGAGCAGCTGCAAACGACTAAAGA--AGAG-T
      300     310     320     330     340     350

      340     350     360     370     380     390
inputs CTGGAGCCGCGCCAGCTGGGATCCAGGCCCTCCTCAGTCGGCAGCCAAGCCAGGCTGC
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
      CTGGAGCTGTGGCAGCTGCAGCCAGTGTCCCTGCTCAGAGTACAGCCAGAACAGG---AC
      360     370     380     390     400     410

      400     410     420     430     440     450

```


inputs ACTTTATAGACCAGCACCGGGCTGCGCTTATCGCGAGGGTCACAAACGTTGAGTGGCTGC

 ACTTTGTGGACCAGCACAGGCAAGCACTCATTGCCAGGGTCACAGAAGTGGACGGAGTGC
 420 430 440 450 460 470
 460 470 480 490 500 510
 inputs TGGATGCTCTGTACGGGAAGGTCCTGACGGATGAGCAGTACCAGGCAGTGGCGGCCGAGC

 TGGATGCTTTGCATGGCAGTGTGCTGACTGAAGGACAGTACCAGGCAGTTCGTGCAGAGA
 480 490 500 510 520 530
 520 530 540 550 560 570
 inputs CCACCAACCCAAGCAAGATGCGGAAGCTCTTCAGTTTCACACCAGCCTGGAACCTGGACCT

 CCACCAGCCAAGACAAGATGAGGAAGCTCTTCAGCTTTGTTCCATCCTGGAACCTGACCT
 540 550 560 570 580 590
 580 590 600 610 620 630
 inputs GCAAGGACTTGCTCCTCCAGGCCCTAAGGGAGTCCCAGTCTACCTGGTGGAGGACCTGG

 GCAAGGACTCCCTCCTCCAGGCCCTGAAGGAAATACATCCCTACTTGGTGATGGACCTGG
 600 610 620 630 640 650
 640 650 660 670 680
 inputs AGCGGAGCTGAGGC-TCCTTCCCAGCAACACTCCGGTC-AGCCCCTGGCAAT-CCCAC-C

 AGCAGAGCTGAGGTATCTTTCCAGCTACATT--ATCTAGCTCCTGACTTTGTATACAC
 660 670 680 690 700 710
 690 700 710 720 730 740
 inputs AAATCATCCTGAATCTGATCTTTTATACACAATATACGAAAAGCCAGCTTGAA

 AATTTTGAACCAATT-TGTATTTGTGTTTAAAAAAAAAAAAAAAAAAGG
 720 730 740 750 760

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ALIGN calculates a global alignment of two sequences
 version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
 > hCARD5-protein 195 aa vs.
 > mCARD5-protein 193 aa
 scoring matrix: paml20.mat, gap penalties: -12/-4
 71.8% identity; Global alignment score: 712

```

      10      20      30      40      50      60
inputs MGRARDAILDALENLTAEELKKFKLLSVPLREGYGRIPRGALLSMDALDLTDKLVSFY
      .....
      MGRARDAILDALENLSGDELKKFKMKLLTVQLREGYGRIPRGALLQMDAIDLTDKLVSY
      10      20      30      40      50      60

      70      80      90     100     110     120
inputs LETYGAELTANVLRDMGLQEMAGQLQAATHQGSGAAPAGIQAPPQSAAKPGLHFIDQHRA
      .....
      LESYGLELTMTVLRDMGLQELAEQLQT-TKEESGAVAAAAASVPAQSTARTG-HFVDQHRQ
      70      80      90     100     110

      130     140     150     160     170     180
inputs ALIARVTNVEWLLDALYGKVLTDQYQAVRAEPTNPSKMRKLSFTPAWNWTCKDLLLQA
      .....
      ALIARVTEVDGVLDALHGSVLTEGQYQAVRAETTSQDKMRKLSFVPSWNLTCCKDSLLQA
      120     130     140     150     160     170

      190
inputs LRESQSYLVEDLERS
      ...
      LKEIHPYLVMDLEQS
      180     190

```

Variable	Mean	SD	Min	Max
Age	38.5	12.5	18	65
Gender	0.5	0.5	0	1
Marital status	0.5	0.5	0	1
Education	12.5	2.5	8	16
Income	15.5	10.5	5	35
Health status	0.5	0.5	0	1
Smoking status	0.5	0.5	0	1
Alcohol consumption	0.5	0.5	0	1
Exercise frequency	0.5	0.5	0	1
Stress level	0.5	0.5	0	1
Sleep quality	0.5	0.5	0	1
Work satisfaction	0.5	0.5	0	1
Life satisfaction	0.5	0.5	0	1
Overall health	0.5	0.5	0	1
Physical health	0.5	0.5	0	1
Mental health	0.5	0.5	0	1
Social health	0.5	0.5	0	1
Emotional health	0.5	0.5	0	1
Behavioral health	0.5	0.5	0	1
Environmental health	0.5	0.5	0	1
Occupational health	0.5	0.5	0	1
Financial health	0.5	0.5	0	1
Family health	0.5	0.5	0	1
Community health	0.5	0.5	0	1
National health	0.5	0.5	0	1
Global health	0.5	0.5	0	1

.....

.....

1 M A S E G A S S E

10 ▶ I I E K Q R T K L L S V L Q Q D P D S I L D

31▶ T L T S R R L I S E E E Y E T L E A I T D

53 P L K K S R K L L I L I Q K K G E D S C C C

75 ▶ F L K C L S N A F P Q S A S T L G L K Q E V

96▶ P R Q G T G E V V E V S R G L E D P F S L

L18▶G T I T P E I A E L S E E K E C P G L G A P

L40▶ E F F T C K E S S H R E P E V P S W E N Q E

161 G R G A Q Q V T A P R S V K G V E Y E V P

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716 CAAGTATCTCCCTCTTAAGCGACGGGCAGAGATACGAGGAGCCAGATGATTGCTGTACTTAGAA
 GTTCATAGAGGGAGAATTGCGTGCCCGTCTCTATGCTCCTCGGTCTACTAAGCGACATGAATCTT
 183▶ A S I S L L S D G Q R Y E E P D D S L Y L E

781 GAAGGGGAAGGTGAAGAGTCTCTGGGTACCCCTGAAGATGTTTGGAGGAAGGGGCCGGCGATGA
 CTTCCCTTCCACTTCTCAGAGAACCCATGGGACTTCTACAAAACCTCCTTCCCGGCCGCTACT
 205▶ E G E G E E S L G Y P E D V L E E G A G D D

846 CCCACAGTGTCTTGTATATGATAGTGAGGAGGAATGCGAGTATGAGGAAAACATGGGCTCTCCG
 GGGTGTACGAAACATATACTATCACTCCTCCTTACGCTCATACTCCTTTTGTACCCGAGGAGGC
 226▶ P Q C F V Y D S E E E C E Y E E N M G S S

911 GTGAAGACAGTAGCTGCGACGACACTTCAGAGACCTGCGTTCCATTGGAAGGGGAGAAAAGCGCT
 CACTTCTGTCAATCGACGCTGCTGTGAAGTCTCTGGACGCAAGGTAACCTTCCCTCTTTTCGCGA
 248▶ G E D S S C D D T S E T C V P L E G E K S A

976 GAAGAAAGAAAAAGAGTGTCTTCAACACGTCCTGTCTGTTGAACATGGATAGAAACAGAAAGCT
 CTTCTTTCTTTTCTCACAAGTTGTGCAGGACAGGACAAACTTGTACCTATCTTTGTCTTTTCGA
 270▶ E E R K R V F Q H V L S C L N M D R N R K L

1041 TCTCCAGAGTTTCGTGAGGCAGTTTTCATAGACCGAGGATGTGAGTGGACACCCAAGACCCAG
 AGAGGGTCTCAAGCACTCCGTCAAAAGGTATCTGGCTCCTACACTCACCTGTGGGTTCTGGGGTC
 291▶ L P E F V R Q F S I D R G C E W T P K T P

1106 GAGACTTAGCTTGAATTTCTTGATGAAAGTTTCAGGCTTTAGACTCGACAGCCAGAGATTCTATC
 CTCTGAATCGAACCTTAAAGAACTACTTTCAAGTCCGAAATCTGAGCTGTGGTCTCTAAGATAG
 313▶ G D L A W N F L M K V Q A L D S T A R D S I

1171 CTGAGGCCCCGAGGTGGCGGGTGAAGAGAATGAAGAATTGCCGGCTGGAATAGAGAAGTTAGGCAT
 GACTCCGGGCTCCACCGCCCACTTCTCTTACTTCTTAACGGCCGACCTTATCTCTTCAATCCGTA
 335▶ L R P E V A G E E N E E L P A G I E K L G I

1236 TGGAGACCCCCAAACCATCCATCCCCTGGATGTCCTCTGCGCCTGCATGCTTTTGTGCAGACAGCT
 ACCTCTGGGGGTTTGGTAGGTAGGGGACCTACAGGAGACGCGACGTACGAAACACGCTCTGTCTGA
 356▶ G D P Q T I H P L D V L C A C M L C A D S

1301 CCTTGCAGCGTGAAGTCATGTCAAACATGTACCAATGCCAGTTTGTCTCTTCCCTGCTACTGCCA
 GGAACGTCGCACTTCAGTACAGTTTGTACATGGTTACGGTCAAACGAGAAGGGGACGATGACCGT
 378▶ S L Q R E V M S N M Y Q C Q F A L P L L L P

1366 GATGCTGAGAACAACAAAAACCTCTTAATGGTAGGGGCCATGAAGGACTTAAAGCAGCCCTCAGC
 CTACGACTCTTGTTGTTTTTGGAGAATTACCATCCCCGGTACTTCTGAATTTCGTGGGAGTCTG
 400▶ D A E N N K N L L M V G A M K D L K Q P S A

FIG. 25 (3 of 7)

2211 GGAGCCCAATCAGAGAGCCAGGGGCTCAATGTGACGACAGTCAGAATGCTCCGGTTTTTCATCAGA
CCTCGGTTAGTCTCTCGGTCCCCGAGTTACACTGCTGTGAGTCTTACGAGGCCAAAAGGTAGTCT
... 681▶ E P I R E P G A Q C D D S Q N A P V F H Q

2276 CTCCAGTATACATGCCCTTATCCAGCACACCCATGGGCTTTGGCCATCAAAAGCTGGAGGTAACTTT
GAGGTCATATGTACGGAATAGGTCGTGTGGGTACCCGAAACCGTAGTTTCGACCTCCATTGAAA
703 T P V Y M P Y P A H P W A L A I K A G G N F

2341 TACCACGTTCCCTTTGAATGCCCCCTGGTTATGGGCTCCCACTTTGGATCAGACAGAGGGGCTAAG
ATGGTGCAGGAAACTTACGGGGGACCAATACCCGAGGGTGAAACCTAGTGTGCTCTCCCAATTC
725 Y H V P L N A P W L W A P T L D H S R G L S

2406 TGGTTCCTTTCCATTTCCCATGCTAAACCCACTCACTCTAAGGCCTTCCAAGCTAACTGCCACCATC
ACCAAGAAAGGTAAGGGTACGATTTTGGGTGAGTGAGATTCCGGAAGGTTTCGATTGACGGTGGTAG
746 G S F H S H A K P T H S K A F Q A N C H H

2471 CCCATCCCTCCCATGCTAAACCCACTCATGTGAATCCCTCTCATGTAAACCCACTCATGTGCAG
GGGTAGGGAGGGTACGATTTGGGTGAGTACACTTAGGGAGAGTACGATTGGGGTGAGTACACGTC
768 P H P S H A K P T H V N P S H A N P T H V Q

2536 CCTTGCATGCTAAACCCACTCACTCTAAGGCCTTCCAAGCTAAACCCACTCCCTCTCAGACCTCT
GGAACGTACGATTTGGGTGAGTGAGATTCCGGAAGGTTCCGATTTGGGTGAGGGAGAGTCTGGAGA
790 P C M L N P L T L R P S K L N P L P L R P L

2601 TGGAGCCAAGCTAACTGCAATCATGCCCATCCCTCCCTTGCTAAACCCCTCTCATACGAATCCCTC
ACCTCCGTTTCGATTGACGTTAGTACGGGTAGGGAGGGAACGATTTCGGAGAGTATGCCTTAGGGAG
811▶ G A K L T A I M P I P P L L N P L I R I P

2666 TGATGCTAACCCCACTCATGTGCGAGCCTTCCCATGCTAAACCCGCTCATCTACAGTCTTCCCAA
ACTACGATTGGGGTGAGTACAGTCGGAAGGGTACGATTGGGCGAGTAGATGTCAGAAGGGTTT
833 L M L T P L M C S L P M L N P L I Y S L P K

2731 CAAAACCCCTCCCAATCCCAATCTACTGCAGTTTCACGGCACACAACCTCAGCAGTCCCAGTCTAA
GTTTTTCGGAGGGGTAGGGTTAGATGACGTCAAGTCCCGTGTGTTTGAGAGTCGTACAGGTCAGATT
855▶ Q N N P P H P N L L Q F T A H K P Q Q S Q S K

2796 GCCTTCTCTCAGCAGAGACCCAGTCAGCCTAAATCATTTCCAGACCAAGCCCTTCACAGGCCAGGGCCT
CGGAAGAGTCGTCTCTGGGTCAGTCGGATTTAGTAAGGTCGGTTCCGAAGTGTCCCGTCCCGGA
876▶ P S Q Q R P S Q P K S F Q T K P S Q A R A

FIG 25 (5 of 7)

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3706 GCCACTGAGCAGATACTCTGCACCATTTGGTACAGTTAAATCAGCTTGCTTCTGGTAATAGCCCCA
CGGTGACTCGTCTATGAGACGTGGTAACCATGTCAATTTAGTCGAACGAAGACCATTATCGGGGT

3771 ATCTACCACATTTATCCCTTACAGGCGGAAATAATGAATGATCAGCAAAACATCCAATTTTACCT
TAGATGGTGTAAATAGGGAATGTCCGCCCTTTATTACTTAGTTCGTTTTGTAGGTTAAATGGA

3836 TAACCTTGGTACTGATTTGTATATGTATCATTCTTTATATAATAGCTAAGAAAAATTTAGCTCATT
ATTGGAACCATGACTAAACATATACATAGTAAGAAATATATTATCGATTCTTTTAAATCGAGTAA

3901 AGGGGTTCTGATATATTAGTTTAAATGGTTTGAAGTCAGAAATGTGTTAGTTTTTAAATTTAGAGT
TCCCCAAGACTATATAATCAAATACCAAACCTTCAGTCTTTACACAATCAAAAATTTAAATCTCA

3966 TAATTGAAAAATATTGAGATGAATTTACAAAGGCTATAAGTAATGTTTGAGAGGGTTATAATTTTT
ATTAACCTTTTATAACTCTACTTAAATGTTTCCGATATTCATTACAAACTCTCCCAATATTAAAAA

4031 GTAGACTCATACTGTTCTGAACATTTGGATAGCTTCTCGTAGTTAGCAGTGTATAGAAGAATAT
CATCTGAGTATGACAAGACTTGTAAACCTATCGAAGAGCATCAATCGTCACAATATCTTCTTATA

4096 ATTTGATTTCAGGTATTTAACCAGAGCTGCTCTTAGTTTTTAAAGTGTACCAAGAGTCAATAAAAG
TAAACTAAGTCCATAAATGGTCTCGACGAGAATCAAAAATTCACAGTGGTTCTCAGTTATTTTT

4161 GCTACATTATCTGAACATGTGGGAACACAACCTGTGACCTTACACTTAAGAGACTGAGGAAGGGAA
CGATGTAATAGACTTGTACACCCCTGTGTTGACACTGGAATGTGAATTTCTCTGACTCCTTCCCTT

4226 ATCAAGGTTCAAGCCAGCAGCATAGTGAGACCAGGTCTCAAGACAAAACTATCCACCTTA
TAGTTCCAAGTTCGGTCTGCTGTATCACTCTGGTCCAGAGTTCTGTGTTTTTGATAGGTGGAAT

4291 AGGAAGATTTTAAATTTGCCTCATTAAAGAAATAAGTAAGATTTATAAATTTGACTAAATGTCA
TCCCTCTAAAAATTTTAAACGGAGTAATTCCTTTATTTTCATTCTAAATATTTAACCTGATTTACAGT

4356 CATCTTTGAACCTTATGACTGTTTAAATTTTTGACTTAAAGTTTAAATTTTATTATTGTATGCGTGT
GTAGAAACTTTGAATACTGACAAATTAaaaaactgaatttcaaattaaaaataataacatacgcac

4421 GTTGTATGTGTGTCACATGTGTCCACTGCATGTATGTGAGGCCATCAGACAATGTTGTAGAG
CAACATACACACACGTGTACACACGGTGACGTACATACACCTCCGGTAGTCTGTTACAACATCTC

4486 TCTGTTCTTTTCTCTTAGCCCTATGTGTTTTACCCACTGAGCTAGGCCACCTACTCCTATAAGTC
AGACAAGAAAGGAGAATCGGGATACAAAAATGGGTGACTCGATCCGGTGGATGAGGATATTGAG

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4551 TAATTTTAAATAGTAAATAGTTCTAAGAAGTCAATCAGGGAAAAAATGGCTGTCAAAGTCTCA
ATTAAAAATTATCATTTTATCAAGATTCTTCAGTTAGTCCCTTTTTTTACCGACAGTTTCAGAGT

4616 AAGAAAAATCGTATTAGCCATGGATAGAGACTCACCTCTTGAATCATTTGTGTCTGAGAATAGCC
TTCTTTTTTAGCATAAATCGGTACCTATCTCTGAGTGGGAGAACTTAGTAAACACAGACTCTTTATCGG

4681 TAATATCACAATAATGTGTTTGTACATGTGTTAGTTAATATTGTTTTTCAGAGTATTTAATCTCTC
ATTATAGTCTTATTACACAAACATGTACACAATCAATTATAACAAAAGTCTCATAAATTAGAGAG

4746 ATGATTATTGTAAAGATGAAAAAGAAATAGTGGCAATGTATGTGAGTATTTAATTTTTGCCTGA
TACTAATAACATTTCTACTTTTTCTTTATCACCCGTTACATACACTCATAAATTAAAACGGACT

4811 CAATTCTGTCTTTTAGAATGATAAATGTAAGAAGTAAAAATAAACGGTTCTCTCAGAACAACT
GTTAAGACAGAAAACTCTACTATTTACATTCTTCATTTTATTTTCCCAAGTAAGAGTCTTGTTC

4876 AAGCCAGCTCACTTAAGTCTGGGCCCTGCTGGCATTGGCTAGTCTAGCTACCCCCACCCAAACAC
TTCCGGTCGAGTGAATTTCAGACCCGGGACGACCGTAACCGATCAGATCGATGGGGGTGGGTTTGTG

4941 AAAAGTTTAGAGAAGAAAAAGACTGAGTCAAGCTTGCCTAATGACTTTTGGACATAAAGTTTATG
TTTTCAAATCTCTCTTTTACTGACTCAGTTTCAACGGATTACTGAAAACCTGTATTTCAAATAC

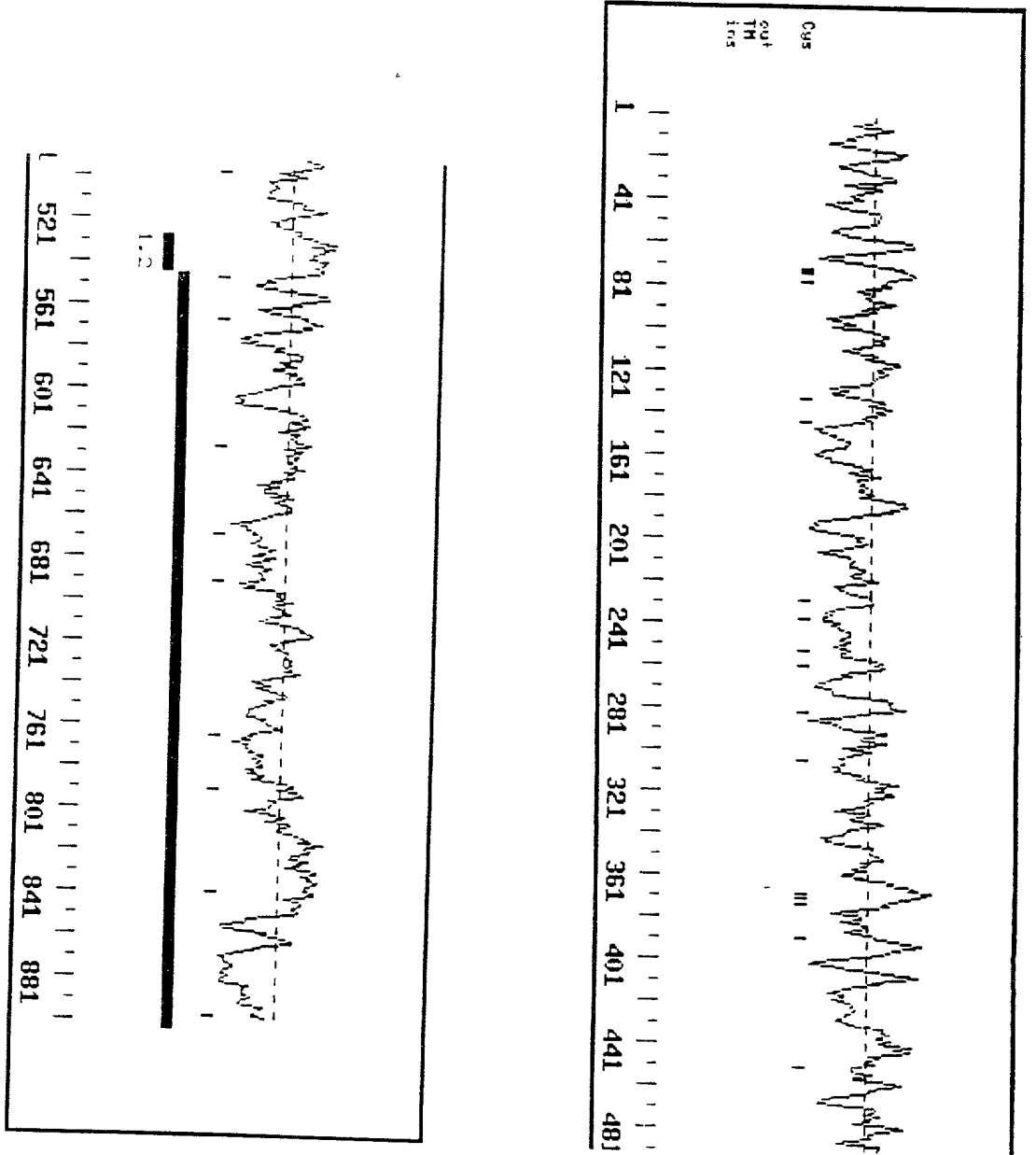
5006 GTCTAGAAAGCCTTAAAAAAGTAGGATATAAAACATGTAAATTAACCCACACATTATGTGGGT
CAGGATCTTTTCGGAATTTTATTCATCTATATTTTGTACATTTAATTGGGTGTGTAATACACCCA

5071 TGAGAAGCAGAAAAATGTCAGTAGAACACTCGGCCAGTGCATAAAGAAGGAAGAGACCTCTGTTT
ACTCTTCGTCTTTTTTACAGTCATCTTGTGAGCCGGTCACGTATTTCTTCCCTTCTCTGGAGACAAG

5136 TGGGTTATAAAACTGCTCTTTGTGCTCAATTGTCCCTGCTTTTGTTTGCCAGAATGTACAAGA
ACCCAATATTTTGACGAGAAACACGAGTTAAACAGGGGACGAAAACAAACGGTCTTTACATGTTCT

5201 TTATAAAATAAACTCACTTTTACTTTTTAAAAAAGGGCGG
AATATTTTATTTGAGTGAAATGAAATTTTTTTTTTTTTTTTTTCCCGCC

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FIG. 26

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	- - - -	G X H F X D Q H R X A L I A R V T X V X X V L D A L Y - G X V L T E X Q	Majority
		10 20 30 40	
1		M E A R D K Q V L R S L R L E L G A E V L V E G L V L Q Y L Y Q E G I L T E N H	RAIDD
1	- - - -	G L H F I D Q H R A A L I A R V T N V E W L L D A L Y - G K V L T D E Q	hCARD5
1	- - - -	G - H F V D O H R Q A L I A R V T E V D G V L D A L H - G S V L T E G Q	mCARD5
		Y Q A V R A E T T X X X K M R K L F S F X P S W N X T C K D X L L Q A L X E X X	Majority
		50 60 70 80	
41		I Q E I N A Q T T G L R K T M L L L D I L P S R G P K A F D T F L D S L Q E F -	RAIDD
36		Y Q A V R A E P T N P S K M R K L F S F T P A W N W T C K D L L L Q A L R E S Q	hCARD5
35		Y Q A V R A E T T S Q D K M R K L F S F V P S W N L T C K D S L L Q A L K E I H	mCARD5
		P Y L V E D L E X S - - - - -	Majority
		90	
80		P W V R E K L K K A R E E A M	RAIDD
76		S Y L V E D L E R S	hCARD5
75		P Y L V M D L E Q S	mCARD5

FIG 27

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CACGCGTCCGCCGATCAGAGAGTGCTCCGAGCTGGGTTGCCCACTGTGCTTGTATCTGCACTCTCCAACACTAGGC 79
 ATCATTGACATGTTAAAGCTTAGCCAAATAGAATTGTCTTTGTCACTCTTTTTTAACTTTTACTTATTCATTAGGAT 158
 M A T E S T P S E 9
 GATTTTATAATATATTTCTCGTTTATAGAGAAACAGGAACA ATG GCT ACC GAG AGT ACT CCC TCA GAG 226
 I I E R E R K K L L E I L Q H D P D S I 29
 ATC ATA GAA AGA GAA AGA AAA AAG TTG CTT GAA ATC CTT CAA CAT GAT CCT GAT TCT ATC 286
 L D T L T S R R L I S E E E Y E T L E N 49
 TTA GAC ACG TTA ACT TCT CGG AGG CTG ATT TCT GAG GAA GAG TAT GAG ACT CTG GAG AAT 346
 V T D L L K K S R K L L I L V Q K K G E 69
 GTT ACA GAT CTC CTG AAG AAA AGT CGG AAG CTG TTA ATT TTG GTA CAG AAA AAG GGA GAG 406
 A T C Q H F L K C L F S T F P Q L A A I 89
 GCG ACC TGT CAG CAT TTT CTC AAG TGT TTA TTT AGT ACT TTT CCA CAG TTA GCT GCC ATT 466
 C G L R H E V L K H E N T V P P Q S M G 109
 TGC GGC TTA AGG CAT GAA GTT TTA AAA CAT GAG AAT ACA GTA CCT CCT CAA TCT ATG GGG 526
 A S S N S E D A F S P G I K Q P E A P E 129
 GCA AGC AGT AAT TCA GAA GAT GCT TTT TCT CCT GGA ATA AAA CAG CCT GAA GCC CCT GAG 586
 I T V F F S E K E H L D L E T S E F F R 149
 ATC ACA GTG TTC TTC AGT GAG AAG GAA CAC TTG GAT TTG GAA ACC TCT GAG TTT TTC AGG 646
 D K K T S Y R E T A L S A R K N E K E Y 169
 GAC AAG AAA ACT AGT TAT AGG GAA ACA GCT TTG TCT GCC AGG AAG AAT GAG AAG GAA TAT 706
 D T P E V T L S Y S V E K V G C E V P A 189
 GAC ACA CCA GAA GTC ACA TTA TCA TAT TCA GTT GAG AAA GTT GGA TGT GAA GTT CCA GCA 766
 T I T Y I K D G Q R Y E E L D D S L Y L 209
 ACT ATT ACA TAT ATA AAA GAT GGA CAG AGA TAT GAG GAG CTA GAT GAT TCT TTA TAC TTA 826
 G K E E Y L G S V D T P E D A E A T V E 229
 GGA AAA GAG GAA TAT CTA GGA TCT GTT GAC ACC CCT GAA GAT GCA GAA GCC ACT GTG GAA 886
 E E V Y D D P E H V G Y D G E E D F E N 249
 GAG GAG GTT TAT GAT GAC CCA GAG CAC GTT GGA TAT GAT GGT GAA GAG GAC TTC GAG AAT 946
 S E T T E F S G E E P S Y E G S E T S L 269
 TCA GAA ACC ACA GAG TTC TCT GGT GAA GAA CCA AGT TAT GAG GGA TCA GAA ACC AGC CTT 1006
 S L E E E Q E K S I E E R K K V F K D V 289
 TCA TTG GAG GAG GAA CAG GAG AAA AGT ATA GAA GAA AGA AAA AAG GTG TTT AAA GAT GTC 1066
 L L C L N M D R S R K V L P D F V K Q F 309
 CTG TTA TGT TTG AAC ATG GAT AGA AGC AGA AAG GTT CTG CCA GAT TTT GTT AAA CAA TTC 1126
 S L D R G C K W T P E S P G D L A W N F 329
 TCC TTA GAT CGA GGA TGT AAG TGG ACC CCT GAG AGT CCA GGA GAC TTA GCC TGG AAT TTC 1186
 L M K V Q A R D V T A R D S I L S H K V 349
 CTG ATG AAA GTT CAA GCA CGA GAT GTG ACG GCT AGG GAT TCA ATC CTC AGT CAC AAG GTT 1246
 L D E D S K E D L L A G V E N L E I R D 369
 CTG GAT GAA GAT AGC AAG GAG GAT TTG CTG GCT GGA GTG GAG AAT TTG GAA ATT CGA GAC 1306

Fig. 2B (1 of 4)

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I Q T I N P L D V L C A T M L C S D S S 389
ATA CAA ACC ATT AAT CCC CTT GAC GTG CTT TGT GCC ACC ATG CTG TGT TCA GAT AGC TCT 1366

L Q R Q V M S N M Y Q C Q F A L P L L L 409
TTG CAA CGC CAA GTC ATG TCA AAC ATG TAT CAG TGC CAG TTT GCT CTT CCC CTG CTA CTG 1426

P D A E N N K S I L M L G A M K D I V K 429
CCA GAT GCA GAA AAC AAC AAA AGC ATC TTA ATG CTG GGG GCC ATG AAA GAC ATT GTG AAG 1486

K Q S T Q F S G G P T E D T E K F L T L 449
AAG CAG TCA ACA CAG TTT TCA GGG GGG CCT ACA GAG GAT ACA GAA AAG TTT CTG ACT CTC 1546

M K M P V I S F V R L G Y C S F S K S R 469
ATG AAG ATG CCT GTC ATC TCT TTT GTG CGT CTA GGA TAC TGT AGC TTC TCT AAG TCC AGA 1606

I L N T L L S P A Q L K L H K I F L H Q 489
ATC CTC AAC ACA CTT CTC AGC CCT GCC CAG TTG AAA TTA CAC AAA ATC TTT CTT CAT CAA 1666

D L P L L V L P R Q I S D G L V E I T W 509
GAT TTG CCT CTT TTG GTG CTT CCC CGG CAA ATC TCT GAT GGC CTG GTT GAG ATA ACA TGG 1726

C F P D S D D R K E N P F F Q K P V A L 529
TGT TTT CCT GAT AGC GAT GAT AGA AAG GAA AAC CCC TTT TTC CAA AAG CCT GTT GCT CTG 1786

A N L R G N L E S F W T Q F G F L M E V 549
GCT AAT CTC CGT GGA AAT CTA GAA AGT TTT TGG ACT CAG TTT GGT TTT TTG ATG GAA GTT 1846

S S A V F F F T D C L G E K E W D L L M 569
TCT TCA GCT GTG TTT TTT TTC ACT GAC TGT TTA GGT GAG AAG GAA TGG GAC TTG CTA ATG 1906

F L G E A A I E R C Y F V L S S Q A R E 589
TTT TTA GGA GAG GCT GCC ATT GAA AGA TGC TAC TTT GTT CTC AGT TCC CAA GCC AGG GAG 1966

S E E A Q I F Q R I L N L K P A Q L L F 609
AGT GAA GAG GCT CAA ATT TTT CAG AGG ATA CTG AAC TTG AAG CCA GCA CAG CTA CTG TTT 2026

W E R G D A G D R R K N M E G L Q A A L 629
TGG GAG AGG GGA GAT GCT GGG GAT AGA AGG AAG AAC ATG GAG GGC CTT CAA GCT GCC CTC 2086

Q E V M F S S C L R C V S V E D M A A L 649
CAG GAA GTG ATG TTC TCT TCT TGC CTC AGA TGT GTG TCT GTG GAG GAT ATG GCC GCC CTG 2146

A R E L G I Q V D E D F E N T Q R I Q V 669
GCC AGG GAG CTG GGG ATT CAG GTA GAT GAA GAC TTT GAA AAC ACT CAG AGA ATT CAA GTT 2206

S S G E N M A G T A E G E G Q Q R H S Q 689
TCC TCT GGA GAA AAC ATG GCT GGG ACA GCT GAA GGT GAG GGT CAG CAA AGA CAC AGT CAG 2266

L K S S S K S Q A L M P I Q E P G T Q C 709
CTA AAA AGC TCA TCT AAA AGC CAG GCT CTA ATG CCA ATT CAA GAG CCT GGG ACT CAA TGT 2326

E L S Q N L Q N L Y G T P V F R P V L E 729
GAG CTC AGC CAG AAT CTT CAG AAT CTC TAT GGT ACC CCA GTA TTC AGG CCT GTT CTA GAG 2386

N S W L F P T R I G G N F N H V S L K A 749
AAC TCC TGG CTC TTT CCA ACC AGA ATT GGA GGT AAC TTT AAC CAT GTT TCC TTG AAA GCC 2446

S W V M G R P F G S E Q R P K W F H P L 769
TCC TGG GTT ATG GGC CGC CCC TTT GGG TCA GAG CAG AGG CCT AAG TGG TTC CAT CCT TTG 2506

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P F Q N A G A Q G R G K S F G I Q S F H 789
CCT TTT CAG AAT GCA GGG GCC CAG GGC CGA GGT AAA AGT TTT GGT ATT CAA TCC TTC CAT 2566

P Q I F Y S G E R F M K F S R V A R G C 809
CCC CAG ATA TTT TAT TCA GGT GAA AGA TTC ATG AAA TTT TCC AGA GTT GCT CGG GGA TGT 2626

H S N G T F G R L P R P I C Q H V Q A C 829
CAC TCG AAT GGA ACA TTT GGG AGA CTG CCA AGA CCC ATT TGT CAG CAT GTA CAG GCC TGC 2686

P E R P Q M M G T L E R S R A V A S K I 849
CCT GAG AGA CCA CAA ATG ATG GGA ACT CTT GAA AGG TCT AGG GCA GTA GCC TCC AAG ATA 2746

G H S Y S L D S Q P A R A V G K P W P Q 869
GGT CAC TCC TAT TCC CTG GAT TCA CAG CCA GCA AGA GCA GTA GGG AAG CCA TGG CCT CAG 2806

Q A C T R V T E L T E A T G K L I R T S 889
CAA GCT TGC ACC AGG GTA ACA GAG TTA ACT GAA GCA ACT GGA AAA CTG ATA AGA ACA TCC 2866

H I G K P H P Q S F Q P A A A T Q K L R 909
CAT ATT GGA AAG CCT CAC CCT CAG TCC TTT CAA CCA GCA GCA GCC ACA CAA AAA CTA AGA 2926

P A S Q Q G V Q M K T Q G G A S N P A L 929
CCT GCT TCT CAG CAA GGA GTC CAG ATG AAG ACA CAA GGT GGG GCT TCA AAT CCA GCT CTC 2986

Q I G S H P M C K S S Q F K S D Q S N P 949
CAA ATA GGG TCC CAT CCC ATG TGC AAG AGC TCT CAG TTC AAA TCC GAT CAG TCC AAC CCA 3046

S T V K H S Q P K P F H S V P S Q P K S 969
TCC ACA GTC AAA CAC TCC CAG CCT AAA CCC TTC CAT TCT GTG CCC TCT CAA CCT AAA TCC 3106

S Q T K S C Q S Q P S Q T K P S P C K S 989
TCT CAG ACA AAA TCC TGT CAG TCC CAG CCC TCC CAA ACT AAA CCT TCT CCA TGC AAA TCT 3166

T Q P K P S Q P W P P Q S K P S Q P R P 1009
ACT CAG CCT AAG CCA AGC CAG CCC TGG CCT CCC CAG TCT AAG CCT TCT CAG CCC AGA CCC 3226

P Q P K S S S T N P S Q A K A H H S K A 1029
CCT CAA CCT AAG TCA TCC TCA ACC AAT CCT TCA CAA GCT AAG GCA CAC CAC TCA AAA GCA 3286

G Q K R G G K H * 1038
GGG CAG AAG AGG GGA GGG AAG CAT TAA 3313

AGAGCTAACTCCAGAGATCTATAAAGCATATCCTTTACCCAGGCCATTCTCTATCATATAGTAAGCAGAAGAGTTGCCAT 3392

GAAAGTAAAAGACTACTGTGTCATTAGCATGTAAAACAAAGAAAGATATACATGACCGAATTGGATATCTTTGTTTGTGTTG 3471

TTTGAGACAGAGTTTCACTCTTGTGTTGCCAGGCTGGAGTGCAATGGCAGCATCTCGGCTCACCGCAACCTCTGCTTCCT 3550

GGCTTAAAGTGATTCTCCTGCCTCAGCCTCTCGAGTAGCTGGGATTACAGGCATGCACCACCACACCCAGCTAATTTTG 3629

TATTTTAGTAGAGGCAGGGTTTCTCCATGTTGGTCAGGCTGGTCTTGAACCTCCCGACCTCAGGTGATCCGCCCCACCTA 3708

GGCCTCTCAAAGTGTTGGGATTACGTGTGTAAAGCCACAGTGCCCGAGCCGAATTGGATATCTTTAAGATATCTGTAAGT 3787

GTTATATCCCTAACCAAGAAGAAAAATATGAAAATAATTAAGACTAGAATCAAGCAGTAGATAATTGAATCCAATCTTG 3866

GGTATTATTAGATAATGTATAACTTGCACCCAGGGAATGGGGTCTATGAGACAACCCCACTTGAGAGAAGATGGGGTT 3945

AGGGTCTCTAATTGCAAAGTACTGTACAATAGGACGAAAGTTGCCTCTGTGTCTGAGAAAGTATCTTAGTTGTTGGCT 4024

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GCTCCAGAGGTATCTTTGTCAAAGCTTCTGGTTCAATATCAGCCACTGAGCAGATAACCCTGCTTATTGGTGTGGTT 4103
AAATCAACTAGCTTCTGCTAATAGCCCCAATTTGCTTGAATGGGAAAACTCTCTCATTGACCCCTTATAGGTAGAAATA 4182
ATGAATTAACAACCAATAAAATTAATCATTGGCATTAAAAAAAAAAAAAAAAAAAAA 4244

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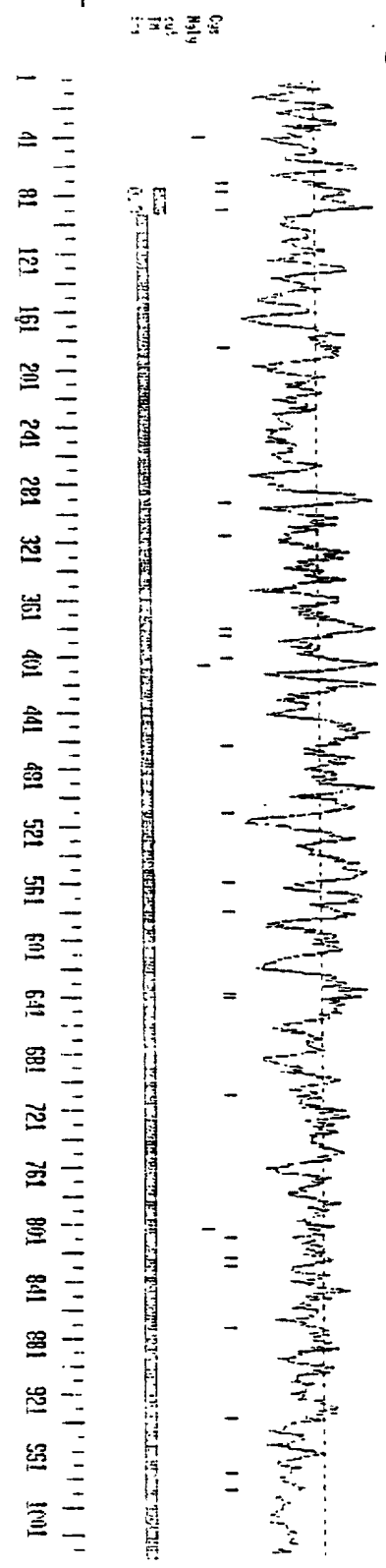


FIG. 29

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FIG. 31